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Applicant : Goddard, et al.
App. No : 10/063,540
Filed : May 2, 2002
For : ANTIBODIES TO A POLYPEPTIDE
ENCODED BY A NUCLEIC ACID
UNDEREXPRESSED IN
ESOPHAGEAL TUMOR AND
MELANOMA
Examiner : Seharaseyong, J.
Art Unit : 1647

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September 29, 2005

(Date)

AnneMarie Kaiser, Reg. No. 37,649

Mail Stop Appeal Brief - Patents

Commissioner for Patents

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Alexandria, VA 22313-1450

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(X) Appeal Brief in 47 pages.

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FEE CALCULATION				
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Appeal Brief	41.20(b)(2)	1402 (\$500)		\$500
1 Month Extension	1.17(a)(1)	1251 (\$120)		\$
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(X) A copy of evidence cited in Appellant's Brief and listed in Appendix B.

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Docket No. : GNE.3230R1C27

Customer No.: 30,313

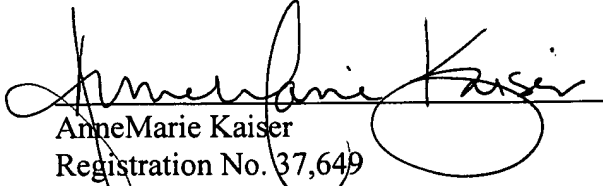
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Filing Date : May 2, 2002

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

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ON APPEAL TO THE BOARD OF PATENT APPEALS AND INTERFERENCES
APPELLANT'S BRIEF

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Mail Stop Appeal Brief – Patents
 COMMISSIONER FOR PATENTS
 P.O. Box 1450
 Alexandria, VA 22313-1450

Dear Sir:

The Applicants appeal the rejection of Claims 1-5 in the above-captioned patent application. These claims were rejected in a Final Office Action dated March 30, 2005. In response to Applicants' Amendment and Response to Final Office Action, the Examiner issued an Advisory Action dated June 17, 2005. Applicants mailed a Notice of Appeal August 1, 2005.

I. REAL PARTY IN INTEREST

Pursuant to 37 C.F.R. 41.37(c)(1), Appellants hereby notify the Board of Patent Appeals and Interferences that the real party in interest is the assignee of record for this application, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080.

II. RELATED APPEALS AND INTERFERENCES

A Notice of Appeal has been filed in the related Application Nos. 10/063,653, 10/063,659, 10/063,660, 10/063,661, 10/063,713, 10/063,534, 10/063,540, 10/063,560,

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10/063,578, 10/063,584, 10/063,586, 10/063,587, 10/063,616, 10/063,648, 10/063,652. A Notice of Appeal and an Appeal Brief have also been filed in the related Application Nos. 10/063,578 and 10/063,584. Appellants are unaware of any other related appeals or interferences.

III. STATUS OF THE CLAIMS

The above-captioned application was filed with Claims 1-6. Claim 6 was canceled in an Amendment and Response to Office Action mailed September 27, 2004. Claims 1-5 were finally rejected by the Examiner in a final Office Action mailed March 30, 2005. Appellants mailed an Amendment and Response to Final Office Action on May 27, 2005, amending Claim 1. The Examiner issued an Advisory Action dated June 17, 2005, which did not indicate whether the claim amendment and other evidence submitted in the After Final Amendment would be entered for purposes of appeal. Appellants confirmed in telephone conferences with the Examiner on June 23, 2005, and his Supervisor on August 2, 2005 that the amendments and exhibits were entered by the Examiner. Accordingly, Claims 1-5 are the subject of this appeal. The claims at issue are attached hereto as Appendix A.

IV. STATUS OF AMENDMENTS

Appellants mailed an Amendment and Response to Final Office Action on May 27, 2005, amending Claim 1. The Examiner issued an Advisory Action dated June 17, 2005, which did not indicate whether the claim amendment and other evidence submitted in the After Final Amendment would be entered for purposes of appeal. Appellants confirmed in telephone conferences with the Examiner on June 23, 2005, and his Supervisor on August 2, 2005, that the amendments and exhibits were entered by the Examiner.

V. SUMMARY OF THE CLAIMED SUBJECT MATTER

The claimed subject matter relates to isolated antibodies which specifically bind to the polypeptide having SEQ ID NO: 34. As amended, independent Claim 1 reads:

1. An isolated antibody that specifically binds to the polypeptide of SEQ ID NO: 34.

Various aspects of the claimed antibody are described in the specification at, for example, paragraphs [0024], [0225], [0238]-[0248], and [0361]-[0405]. SEQ ID NO: 34 is disclosed in the Sequence Listing appended to the application.

VI. GROUND OF REJECTION TO BE REVIEWED ON APPEAL

The Examiner has rejected Claims 1-5 under 35 U.S.C. §101, stating that the claimed invention is not supported by either a specific and substantial asserted utility or a well-established utility.

The Examiner has also rejected Claims 1-5 under 35 U.S.C. §112, first paragraph. The Examiner asserts that since the claimed invention is not supported by either a specific or substantial asserted utility or a well-established utility, one skilled in the art clearly would not know how to use the claimed invention.

Claims 1-5 can be considered as a group for purposes of the utility and enablement rejections.

VII. APPELLANTS' ARGUMENT

A. Summary of Arguments

1. Utility Rejection

The first issue before the Board is whether Appellants have asserted at least one "specific, substantial, and credible utility." See *Examination Guidelines* ("Utility Guidelines"), 66 Fed. Reg. 1092 (2001). Appellants have asserted that the claimed antibodies to the polypeptide of SEQ ID NO: 34 (the PRO1277 polypeptide) are useful as diagnostic tools for cancer, particularly for esophageal and skin cancer. This asserted utility is specific, substantial, and credible.

Briefly stated, Appellants' asserted utility is based on the disclosure in Example 18 of the instant application that the mRNA encoding the PRO1277 polypeptide is more highly expressed in normal esophageal and skin tissue compared to esophageal and melanoma tumor, respectively. It is well-established that there is a reasonable correlation between changes in mRNA level for a particular gene and a corresponding change in the level of expression of the encoded polypeptide, such that increasing or decreasing the amount of mRNA for a particular gene leads to a corresponding increase or decrease in the amount of the encoded protein. Thus, one of skill in the art would be more likely than not to believe that, like the PRO1277 mRNA, the PRO1277 protein is more highly expressed in normal esophageal and skin tissue compared to esophageal and melanoma tumor, respectively. This differential expression of PRO1277 polypeptide is

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useful for distinguishing esophageal or melanoma tumor tissue from its normal tissue counterpart. Therefore, the claimed antibodies to the PRO1277 polypeptide have a specific, substantial and credible utility as diagnostic tools for cancer, particularly esophageal and skin cancer, as is explained in more detail below.

2. Enablement Rejection

The second issue before the Board is whether Appellants have enabled the pending claims such that one of skill in the art would be able to make and use the claimed invention. The Examiner has rejected Claims 1-5 under 35 U.S.C. §112, first paragraph, arguing that because the claimed invention is not supported by either a specific or substantial asserted utility or a well-established utility, one skilled in the art clearly would not know how to use the claimed invention. *See First Office Action* at 8; *Final Office Action* at 3.

For the reasons discussed in detail below, the claimed invention is supported by a specific, substantial and credible utility. Because the lack of a supporting utility is the only basis for the Examiner's rejection under 35 U.S.C. § 112, first paragraph, the Board should reverse the rejection of Claims 1-5 as lacking enablement.

B. Utility Rejection – Detailed Arguments

The first issue before the Board is whether Appellants have asserted at least one “specific, substantial, and credible utility.” *See Examination Guidelines*, 66 Fed. Reg. 1092 (2001). Appellants have asserted that the claimed antibodies to the polypeptide of SEQ ID NO: 34 (the PRO1277 polypeptide) are useful as diagnostic tools for cancer, particularly for esophageal and skin cancer. This asserted utility is specific, substantial, and credible, as is explained in more detail below.

1. Utility – Legal Standard

A “specific utility” is defined as utility which is “specific to the subject matter claimed,” in contrast to “a general utility that would be applicable to the broad class of the invention.” *See M.P.E.P.* § 2107.01 I. For example, it is generally not enough to state that a nucleic acid is useful as a diagnostic tool without also identifying the condition that is to be diagnosed.

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The requirement of “substantial utility” defines a “real world” use, and derives from the Supreme Court’s holding in *Brenner v. Manson*, 383 U.S. 519, 534 (1966) stating that “[t]he basic *quid pro quo* contemplated by the Constitution and the Congress for granting a patent monopoly is the benefit derived by the public from an invention with substantial utility.” In explaining the “substantial utility” standard, M.P.E.P. § 2107.01 cautions, however, that Office personnel must be careful not to interpret the phrase “immediate benefit to the public” or similar formulations used in certain court decisions to mean that products or services based on the claimed invention must be “currently available” to the public in order to satisfy the utility requirement. “Rather, any reasonable use that an applicant has identified for the invention that can be viewed as providing a public benefit should be accepted as sufficient, at least with regard to defining a ‘substantial’ utility.” *M.P.E.P.* § 2107.01 (emphasis added).

Indeed, the Guidelines for Examination of Applications for Compliance With the Utility Requirement, set forth in M.P.E.P. § 2107 II(B)(1) gives the following instruction to patent examiners: “If the applicant has asserted that the claimed invention is useful for any particular practical purpose ... and the assertion would be considered credible by a person of ordinary skill in the art, do not impose a rejection based on lack of utility.”

Finally, in assessing the credibility of the asserted utility, the M.P.E.P. states that “to overcome the presumption of truth that an assertion of utility by the applicant enjoys” the PTO must establish that it is “more likely than not that one of ordinary skill in the art would doubt (i.e., ‘question’) the truth of the statement of utility.” *M.P.E.P.* § 2107.02 III A.

2. Utility – Burden of Proof

It is well established that a specification which contains a disclosure of utility which corresponds in scope to the subject matter sought to be patented “must be taken as sufficient to satisfy the utility requirement of § 101 for the entire claimed subject matter unless there is reason for one skilled in the art to question the objective truth of the statement of utility or its scope.” *In re Langer*, 503 F.2d 1380, 1391, 183 U.S.P.Q. 288, 297 (C.C.P.A. 1974). Thus “the PTO has the initial burden of challenging a presumptively correct assertion of utility in the disclosure.” *In re Brana*, 51 F.3d 1560, 1566, 34 U.S.P.Q.2d 1436 (Fed. Cir. 1995). Only after the PTO provides evidence showing that one of ordinary skill in the art would reasonably doubt the asserted utility

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does the burden shift to the applicant to provide rebuttal evidence sufficient to convince such a person of the invention's asserted utility. *Id.*

3. Utility – Standard of Proof

Compliance with 35 U.S.C. § 101 is a question of fact. *Raytheon v. Roper*, 724 F.2d 951, 956, 220 U.S.P.Q. 592, 596 (Fed. Cir. 1983). The evidentiary standard to be used throughout *ex parte* examination in setting forth a rejection is a preponderance of the evidence, or “more likely than not” standard. *In re Oetiker*, 977 F.2d 1443, 1445, 24 U.S.P.Q.2d 1443, 1444 (Fed. Cir. 1992). This is stated explicitly in the M.P.E.P.:

[T]he applicant does not have to provide evidence sufficient to establish that an asserted utility is true “beyond a reasonable doubt.” Nor must the applicant provide evidence such that it establishes an asserted utility as a matter of statistical certainty. Instead, evidence will be sufficient if, considered as a whole, it leads a person of ordinary skill in the art to conclude that the asserted utility is more likely than not true. *M.P.E.P.* § 2107.02, part VII (emphasis in original, citations omitted).

The Court of Appeals for the Federal Circuit has stated that the standard for satisfying the utility requirement is a low one:

The threshold of utility is not high: An invention is “useful” under section 101 if it is capable of providing some identifiable benefit. *See Brenner v. Manson*, 383 U.S. 519, 534, 86 S.Ct. 1033, 16 L.Ed.2d 69 (1966); *Brooktree Corp. v. Advanced Micro Devices, Inc.*, 977 F.2d 1555, 1571 (Fed. Cir. 1992) (“To violate § 101 the claimed device must be totally incapable of achieving a useful result”); *Fuller v. Berger*, 120 F. 274, 275 (7th Cir. 1903) (test for utility is whether invention “is incapable of serving any beneficial end”). *Juicy Whip, Inc. v. Orange Bang, Inc.*, 185 F.3d 1364, 1366, 51 U.S.P.Q. 2d 1700 (Fed. Cir. 1999) (emphasis added).

The low threshold for satisfying the utility requirement is reflected in the standard set by the Federal Circuit for invalidating a patent based on a lack of utility: “[T]he fact that an invention has only limited utility and is only operable in certain applications is not grounds for finding lack of utility. Some degree of utility is sufficient for patentability. Further, the defense of non-utility cannot be sustained without proof of total incapacity.” *Envirotech Corp. v. Al George, Inc.*, 730 F.2d 753, 762, 221 U.S.P.Q. 473 (Fed. Cir. 1984) (emphasis added, citations omitted).

Because the standard for satisfying the utility requirement is so low, requiring total incapacity for a finding of no utility, the M.P.E.P. cautions that:

Rejections under 35 U.S.C. 101 have been *rarely* sustained by federal courts. Generally speaking, in these *rare* cases, the 35 U.S.C. 101 rejection was sustained [] because the applicant ... asserted a utility that could only be true if it violated a scientific principle, such as the second law of thermodynamics, or a law of nature, or was wholly inconsistent with contemporary knowledge in the art. *M.P.E.P.* § 2107.02 III B., citing *In re Gazave*, 379 F.2d 973, 978, 154 U.S.P.Q. 92, 96 (C.C.P.A. 1967) (underline emphasis in original, italic emphasis added).

4. *Appellants Asserted a Specific, Substantial and Credible Utility that is Sufficient to Satisfy the Utility Requirement of § 101*

The claimed subject matter relates to antibodies which specifically bind to the polypeptide having SEQ ID NO: 34. The polypeptide of SEQ ID NO: 34 (referred to as "PRO1277 polypeptide") is encoded by the polynucleotide of SEQ ID NO: 33 (also referred to as DNA56869-1545). *Specification* at ¶¶ [0059-0060]. Appellants have asserted that the claimed antibodies are useful as diagnostic tools for cancer, particularly esophageal and skin cancer.

In "Example 18: Tumor Versus Normal Differential Tissue Expression Distribution" Appellants disclose that the mRNA encoding PRO1277 polypeptide is more highly expressed in normal esophageal and skin tissue compared to esophageal and melanoma tumor, respectively. *Specification* at ¶¶ [0529-0530] and accompanying tables. As explained in paragraph [0530], the differential expression of the PRO1277 mRNA was detected using the well-established technique of quantitative PCR amplification of cDNA libraries isolated from different human normal and tumor tissue samples. To ensure that equivalent amounts of nucleic acid were used in each reaction, the cDNA for β -actin was used as a control.

The specification teaches that identification of the differential expression of a PRO polypeptide-encoding mRNA in one or more tumor tissues as compared to one or more normal tissues of the same tissue type "renders the molecule useful diagnostically for the determination of the presence or absence of tumor in a subject suspected of possessing a tumor." *Specification* at ¶ [0530]. Because it is well established that changes in mRNA levels lead to changes in the level of the encoded protein, one would expect the PRO1277 protein to be differentially expressed in esophageal and skin tumors. The specification states that PRO polypeptides "may also be used diagnostically for tissue typing, wherein the PRO polypeptides of the present invention may be differentially expressed in one tissue as compared to another, preferably in a diseased tissue as compared to a normal tissue of the same tissue type." *Specification* at ¶ [0336].

Likewise, the specification disclose the use of antibodies to PRO polypeptides as diagnostic tools:

[A]nti-PRO antibodies may be used in diagnostic assays for PRO [polypeptide], *e.g.*, detecting its expression (and in some cases, differential expression) in specific cells, tissues, or serum. Various diagnostic assay techniques known in the art may be used, such as competitive binding assays, direct or indirect sandwich assays and immunoprecipitation assays conducted in either heterogeneous or homogeneous phases. *Specification* at [0407].

Taken together, the specification clearly discloses the use of the claimed antibodies as diagnostic tools for cancer, particularly esophageal and skin cancer. This utility is substantial, as one of skill in the art will recognize that the diagnosis of cancer is a “real world” use; it is specific, as the diagnosis of esophageal and skin cancer is not a utility that applies to the broad class of antibodies; and it is credible, as it not a utility “that could only be true if it violated a scientific principle, ...or a law of nature, or [is] wholly inconsistent with contemporary knowledge in the art.” M.P.E.P. § 2107.02 III B., citing *In re Gazave*, 379 F.2d 973, 978, 154 U.S.P.Q. 92, 96 (C.C.P.A. 1967). Because Appellants’ specification contains a disclosure of utility which corresponds in scope to the claimed subject matter, the asserted utility “must be taken as sufficient to satisfy the utility requirement of § 101 for the entire claimed subject matter unless there is reason for one skilled in the art to question the objective truth of the statement of utility or its scope.” *In re Langer*, 503 F.2d 1380, 1391, 183 U.S.P.Q. 288, 297 (C.C.P.A. 1974). Therefore, the burden of establishing a *prima facie* case of lack of utility rests with the PTO. *See, In re Brana*, 51 F.3d 1560, 1566, 34 U.S.P.Q.2d 1436 (Fed. Cir. 1995) (“the PTO has the initial burden of challenging a presumptively correct assertion of utility in the disclosure”).

5. **The Data in Example 18 are Data Regarding Differential mRNA Levels, not Gene Amplification**

Appellants begin by clarifying that the data concerning the differential expression of the PRO1277 gene presented in Example 18 relate to gene expression, **not gene amplification**. The description of Example 18 makes clear that the results were obtained by quantitative PCR amplification of cDNA libraries. It is well known in the art that cDNA libraries are made from mRNA, and reflect the level of mRNA for a particular gene in the source tissue. Thus, Example 18 is reporting a measure of the *expression* of the PRO1277 gene, *i.e.* mRNA levels, not its *amplification*, *i.e.* the number of copies of the PRO1277 gene in the genome.

For this reason, the relationship between gene amplification or aneuploidy (an abnormal number of chromosomes) and the level of gene expression, *i.e.* mRNA levels, is not relevant to the instant application. The distinction between gene amplification and gene expression has been clarified for the Examiner on numerous occasions, as has the irrelevance of any relationship between aneuploidy and gene expression.

Despite this fact, throughout the final Office Action, the Examiner refers to Example 18 as “amplification data.” For example, the Examiner states “[g]iven the increase in amplified DNA (DNA copy number) for PRO 1277....” *Office Action* at 5 (emphasis added).¹ Similarly, the Examiner states that “the instant specification provides no information regarding differential mRNA levels of PRO1277 The specification describes only gene amplification data.” *Id.* at 12 (emphasis added). In rejecting the declaration of Dr. Polakis, the Examiner again states that “the instant specification provides no information regarding differential mRNA levels of PRO1277 Only gene amplification data were presented.” *Id.* 13-14 (emphasis added).

The Examiner also continues to cite Pennica *et al.* (Proc. Natl. Acad. Sci. USA (1998) 95:14717-14722) to teach that “what is often seen is a *lack* of correlation between DNA amplification and increased gene expression” and that “it does not necessarily follow that an increase in gene copy number results in increased gene expression.” *Id.* at 4 and 16 (emphasis added). And although the Examiner agrees that Pennica does not discuss the relationship between the mRNA level and the level of protein expression, the only relationship at issue in the instant application, the Examiner continues to cite Pennica “to show the lack of correlation of between DNA amplification and gene expression.” *Id.* at 16 (emphasis in original). Elsewhere the Examiner states that “one cannot determine from the data in the specification whether the observed ‘amplification’ of nucleic acid is due to increase in copy number, or alternatively due to increase in transcription rates.” *Id.* at 12 (emphasis added).

The Examiner illustrates this confusion by citing Sen *et al.* (Curr. Opin. Oncol. (2000) 12: 82-88) in the first Office Action, where the Examiner stated that:

Cancerous tissue is known to be aneuploid, that is, having an abnormal number of chromosomes (see Sen, 2000, Curr. Opin. Oncol. 12: 82-88). The data presented in the specification were not corrected for aneuploidy. A slight amplification of a

¹ Citations to “*Office Action*” refer to the final Office Action mailed March 30, 2005, unless indicated otherwise.

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gene does not necessarily mean overexpression in a tissue, but can merely be an indication that the cancer tissue is aneuploid. *First Office Action* at 6-7.

Whether or not gene amplification leads to increased gene expression is completely irrelevant to the instant application. Likewise, whether the differential mRNA expression of the PRO1277 gene reported in Example 18 is due to an increase or decrease in copy number, or alternatively due to an increase or decrease in transcription rates is simply not relevant. Appellants have provided reliable evidence that the PRO1277 mRNA is differentially expressed in certain tumors by examining cDNA libraries, not genomic DNA. Whether this differential mRNA expression is due to aneuploidy, changes in gene copy number, transcription rates, a combination of the these, or some other known or unknown cellular mechanism is simply not relevant to Appellants' asserted utility. Regardless of the cause, the differential expression of PRO1277 mRNA and the resulting differential expression of PRO1277 protein can be used as a molecular marker of esophageal and skin cancer to assist in the diagnosis of this disease.

In response to the above arguments, the Examiner has stated that "[t]hese arguments have been fully considered but are found to be partially persuasive because the Office accepts that aneuploidy has no relevance to the differential expression of the cDNA of the instant invention." *Office Action* at 15 (emphasis added). However, the Examiner then goes on to state that Appellants' assertion that the Examiner is confusing the difference between increased copy number, *i.e.* gene amplification, on the one hand, and increased gene expression, *i.e.* increased mRNA levels, on the other was "fully considered but not found to be persuasive." *Office Action* at 16. The Examiner then cites Pennica *et al.* as discussed above.

The issues before the Board will be greatly simplified if an understanding can be reached that the data in Example 18 reflect the level of mRNA for PRO1277 expressed in the tissues tested, *i.e.*, the level of PRO1277 gene expression, and not the number of copies of the PRO1277 gene present in the genome of the tissue tested, *i.e.*, gene amplification. Once this is established, it is clear that the Sen and Pennica references are irrelevant, and Appellants' references and declarations regarding the relationship between mRNA levels and protein levels are of unquestionable relevance.

6. *The Examiner's Arguments*

In the first Office Action, dated August 3, 2004, the Examiner rejected the pending claims, stating "Claims 1-6 are rejected under 35 U.S.C. 101 because the claimed invention is not supported by either a specific, substantial and credible asserted utility or a well established utility." *First Office Action* at 3. This rejection is maintained in the final Office Action. *Office Action* at 3.

To establish a *prima facie* showing that the claimed subject matter lacks utility, the Examiner must "provide[] evidence showing that one of ordinary skill in the art would reasonably doubt the asserted utility." *In re Brana*, 51 F.3d 1560, 1566, 34 U.S.P.Q.2d 1436 (Fed. Cir. 1995). The Examiner has issued a first Office Action, a final Office Action, and an Advisory Action during the prosecution of the instant application. None of these papers provide any evidence that one of ordinary skill in the art would reasonably doubt the asserted utility.

As discussed above, the Examiner has made a number of irrelevant arguments regarding an asserted lack of correlation between gene amplification and an increase in gene expression, as well as the role of aneuploidy in cancer, citing the Sen and Pennica *et al.* references. These arguments are irrelevant for the reasons discussed above, and will not be addressed in any more detail below. The Examiner's remaining arguments are summarized below.

The Examiner states that the "polynucleotide (cDNA)" for PRO1277 is disclosed to be more highly expressed in normal esophagus and skin compared to the esophageal and melanoma tumor based on the PCR amplification of cDNA libraries, and that the use of the molecule for diagnosis is also disclosed. However, the Examiner rejects this utility, stating that "[t]here is no supporting evidence to indicate that the polypeptide encoded by the polynucleotide of the instant invention is more highly expressed in normal tissues compared to their tumor tissue counterparts, and as such one of skilled in the art would conclude that it is not supported by a substantial asserted utility or a well-established utility." *First Office Action* at 5. The Examiner raises essentially two arguments to reject the asserted utility.

First, the Examiner challenges the sufficiency of the data presented in Example 18. The Examiner argues that the evidence of differential expression of the PRO1277 mRNA in esophageal and melanoma tumors is insufficient because it does not teach what the normal level of expression is, it does not indicate how high the expression level is compared to the disease tissue, it lacks statistical correlation, there is no data to compare expression in the normal and

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disease samples, and that because the normal and tumor samples are not from the same person, there is no possibility of direct comparison between the normal and tumor samples. *See First Office Action* at 5-6. The Examiner also cites Hu *et al.* (J. Proteome Res., (2003) 2(4):405-12) to support for his assertion the literature cautions researchers from drawing conclusions based on small changes in transcript expression levels between normal and cancerous tissue. *Final Office Action* at 5, 13, 14, and 16.

Second, the Examiner argues that “polypeptide levels cannot be accurately predicted from mRNA levels,” citing Haynes *et al.* (Electrophoresis, (1998) 19(11):1862-71) and Chen *et al.* (Mol. and Cell. Proteomics, (2002) 1:304-313) for support. *Office Action* at 4, 14, and 16.

Based on these arguments, the Examiner concludes that “[f]urther research needs to be done to determine whether the decrease in PRO1277 cDNA expression compared to normal esophagus or skin tissues supports a role for the peptide in the cancerous tissue; such a role has not been suggested by the instant disclosure.” *Office Action* at 5-6. The Examiner states that this further research requirement makes clear that the asserted utility is not substantial, and therefore the Appellants’ invention is not complete. *Id.* at 6.

7. **The Examiner has not established a Prima Facie case that Claims 1-5 lack Utility**

The above arguments do not satisfy the Examiner’s burden to “provide[] evidence showing that one of ordinary skill in the art would reasonably doubt the asserted utility.” *In re Brana*, 51 F.3d 1560, 1566, 34 U.S.P.Q.2d 1436 (Fed. Cir. 1995). The Examiner has the burden of presenting “countervailing facts and reasoning sufficient to establish that a person of ordinary skill would not believe the Appellant’s assertion of utility.” *M.P.E.P.* at §2107.02 III.A., *citing in re Brana*, 51 F.3d 1560, 1566, 34 U.S.P.Q.2d 1436 (Fed. Cir. 1995) (“Only after the PTO provides evidence showing that one of ordinary skill in the art would reasonably doubt the asserted utility does the burden shift to the Appellant to provide rebuttal evidence”) (emphasis added). With the exception of the Hu *et al.*, Haynes *et al.*, and Chen *et al.* reference, the Examiner’s assertions are not supported by any facts, evidence, or reasoning. Instead, the Examiner simply makes unsupported assertions. As for the three references cited by the Examiner, for the reasons discussed below, they do not support the Examiner’s position. Therefore there is simply no evidence in the record to support the Examiner’s assertion that

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Appellants' asserted utility is not substantial, and the invention is incomplete. Absent some substantial evidence to support his assertions, the Examiner has failed to establish a *prima facie* showing that one of skill in the art would reasonably doubt the asserted utility, and the Board should accept Appellants' disclosed utility as sufficient.

a. The data in Example 18 are sufficient to establish the asserted utility

Appellants turn first to the Examiner's arguments challenging the reliability of the data reported in Example 18. The Examiner argues that Example 18 and the first declaration of Mr. Grimaldi are insufficient to overcome the utility rejection of the pending claims because the specification does not teach what the normal level of expression is, it does not indicate how high the expression level is compared to the disease tissue, it lacks statistical correlation, there is no data to compare expression in the normal and disease samples, and that because the normal and tumor samples are not from the same person, there is no possibility of direct comparison between the normal and tumor samples. *See First Office Action* at 5-6. The Examiner also argues that the literature cautions researchers from drawing conclusions based on small changes in transcript expression levels between normal and cancerous tissue, citing Hu *et al.* (J. Proteome Res., (2003) 2(4):405-12). *Final Office Action* at 5, 13, 14, and 16. None of these unsupported arguments are sufficient to establish a *prima facie* case that one of skill in the art would reasonably doubt the asserted utility.

As an initial matter, Appellants note that the only objection by the Examiner to the data in Example 18 that is supported by any reasoning or evidence is the assertion that the literature cautions researchers from drawing conclusions based on small changes in transcript expression levels between normal and cancerous tissue. The remainder of the objections are not supported by any evidence or reasoning as to why this makes the data in Example 18 insufficient, and therefore they cannot establish a *prima facie* case. *See In re Brana*, 51 F.3d 1560, 1566, 34 U.S.P.Q.2d 1436 (Fed. Cir. 1995) ("Only after the PTO provides evidence showing that one of ordinary skill in the art would reasonably doubt the asserted utility does the burden shift to the Appellant to provide rebuttal evidence.") (emphasis added). Despite this deficiency, Appellants address the Examiner's objections below.

The gene expression data in Example 18 of the specification show that the mRNA associated with protein PRO1277 was more highly expressed in normal esophageal and skin

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tissue compared to esophageal and melanoma tumor, respectively. *See Specification* at ¶ [0530] and accompanying tables. Gene expression was analyzed using standard quantitative PCR amplification reactions of cDNA libraries isolated from different human tumor and normal human tissue samples. *Id.* It is well known in the art that the number of copies of a particular cDNA in the cDNA library is determined by the number of copies of the corresponding mRNA in the sample. Therefore, the cDNA libraries can be used to determine the level of expression of the corresponding mRNA in the tissue.

Appellants have asserted that identification of the differential expression of the PRO1277 polypeptide-encoding gene in tumor tissue compared to the corresponding normal tissue renders the molecule useful as a diagnostic tool for the determination of the presence or absence of tumor. *Id.* In support of this asserted utility, Appellants submitted as Exhibit 2 to their Amendment and Response to Office Action a first Declaration of J. Christopher Grimaldi, an expert in the field of cancer biology. This declaration explains the importance of the data in Example 18, and how differential gene and protein expression studies are used to differentiate between normal and tumor tissue. *See First Grimaldi Declaration.*

In paragraphs 6 and 7, Mr. Grimaldi explains that the semi-quantitative analysis employed to generate the data of Example 18 is sufficient to determine if a gene is over- or under-expressed in tumor cells compared to corresponding normal tissue. He states that any visually detectable difference seen between two samples is indicative of at least a two-fold difference in cDNA between the tumor tissue and the counterpart normal tissue. He also states that the results of the gene expression studies indicate that the genes of interest “can be used to differentiate tumor from normal.” He explains that, contrary to the PTO’s assertions, “[t]he precise levels of gene expression are irrelevant; what matters is that there is a relative difference in expression between normal tissue and tumor tissue.” *First Grimaldi Declaration* at ¶ 7.

This declaration makes clear that since it is the relative level of expression between normal tissue and suspected cancerous tissue that is important, how high the level of expression in normal tissue is, is irrelevant. As to the Examiner’s questions about the reliability and reproducibility of the results, Appellants employed standard techniques which are well-known and accepted by those of skill in the art. Mr. Grimaldi states that if a difference is detected using these techniques, “this indicates that the gene and its corresponding polypeptide and antibodies against the polypeptide are useful for diagnostic purposes...” *Id.* Thus, it is the uncontested

opinion of an expert in the field that the results are reliable enough to indicate that the claimed antibodies are useful as diagnostic tools. As to the Examiner's concerns regarding the number and types of samples used, Mr. Grimaldi states that the samples are pooled samples of normal and tumor tissue, and therefore are more reliable than individual samples. *Id.* at ¶ 5.

The Examiner has also rejected the data because he questions the statistical significance of the data. However, Appellants are not required to prove utility to a statistical certainty, only that it is more likely than not true. *See Nelson v. Bowler*, 626 F.2d 853, 856-57, 206 U.S.P.Q. 881, 883-84 (C.C.P.A. 1980) (reversing the Board and rejecting an argument that evidence of utility was insufficient because it was not statistically significant). Therefore, whether the results are statistically significant or not is irrelevant to establishing the asserted utility.

The Examiner has also cited Hu *et al.* (J. Proteome Res., (2003) 2(4):405-12) for support for its assertion the literature cautions researchers from drawing conclusions based on small changes in transcript expression levels between normal and cancerous tissue. The PTO states that Hu teaches that not all genes with increased expression in cancer have a known or published role in cancer.

In Hu, the researchers used an automated literature-mining tool to summarize and estimate the relative strengths of all human gene-disease relationships published on Medline. They then generated a microarray expression dataset comparing breast cancer and normal breast tissue. Using their data-mining tool, they looked for a correlation between the strength of the literature association between the gene and breast cancer, and the magnitude of the difference in expression level. They report that for genes displaying a 5-fold change or less in tumors compared to normal, there was no evidence of a correlation between altered gene expression and a *known* role in the disease. *See* Hu at 411. However, among genes with a 10-fold or more change in expression level, there was a strong correlation between expression level and a *published* role in the disease. *Id.* at 412. Importantly, Hu reports that the observed correlation was only found among estrogen receptor-positive tumors, not ER-negative tumors. *Id.*

The general findings of Hu are not surprising – one would expect that genes with the greatest change in expression in a disease would be the first targets of research, and therefore have the strongest known relationship to the disease as measured by the number of publications reporting a connection with the disease. The correlation reported in Hu only indicates that the greater the change in expression level, the more likely it is that there is a *published* or *known* role

for the gene in the disease, as found by their automated literature-mining software. Thus, Hu's results merely reflect a bias in the literature toward studying the most prominent targets, and reflect nothing regarding the ability of a gene that is 2-fold or more differentially expressed in tumors to serve as a disease marker.

Hu acknowledges the shortcomings of this method in explaining the disparity in Hu's findings for ER-negative versus ER-positive tumors: Hu attributes the "bias in the literature" toward the more prevalent ER-positive tumors as the explanation for the lack of any correlation between number of publications and gene expression levels in less-prevalent (and, therefore, less studied) ER-negative tumors. *Id.* Because of this intrinsic bias, Hu's methodology is unlikely to ever note a correlation of a disease with less differentially-expressed genes and their corresponding proteins, regardless of whether or not an actual relationship between the disease and less differentially-expressed genes exists. Accordingly, Hu's methodology yields results that provide little or no information regarding biological significance of genes with less than 5-fold expression change in disease. Nowhere in Hu does it say that a lack of correlation in their study means that genes with a less than five-fold change in level of expression in cancer cannot serve as a molecular marker of cancer.

Appellants submit that a lack of known role for PRO1277 in cancer does not prevent its use as a diagnostic tool for cancer. There is a difference between use of a gene for distinguishing between tumor and normal tissue on the one hand, and establishing a role for the gene in cancer on the other. Genes with lower levels of change in expression may or may not be the most important genes in causing the disease, but the genes can still show a consistent and measurable change in expression. While such genes may or may not be good targets for further research, they can nonetheless be used as diagnostic tools. Thus, Hu does not refute the Appellants' assertion that the PRO1277 gene can be used as a cancer diagnostic tool because it is differentially expressed in certain tumors.

Contrary to the Examiner's assertion that one must know what role a gene or polypeptide plays in cancer for it have utility, the PTO's own written policies recognize that the utility of a nucleic acid does not depend on the function of the encoded gene product. The Utility Examination Guidelines published on January 5, 2001 state: "In addition, the utility of a claimed DNA does not necessarily depend on the function of the encoded gene product. A claimed DNA may have a specific and substantial utility because, e.g. it hybridizes near a disease-associated

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gene or it has a gene regulating activity.” (Federal Register, Volume 66, page 1095, Comment 14). Similarly, here the disclosed nucleic acids, as well as the encoded polypeptides and related antibodies, are useful for determining whether an individual has cancer regardless of whether or not they are the cause of the cancer.

The position of the Examiner requiring a known role for PRO1277 in cancer for utility is also inconsistent with the analogous standard for therapeutic utility of a compound where “the mere identification of a pharmacological activity of a compound that is relevant to an asserted pharmacological use provides an ‘immediate benefit to the public’ and thus satisfies the utility requirement.” *M.P.E.P.* §2701.01 (emphasis original). Here, the mere identification of altered expression in tumors is relevant to diagnosis of tumors, and, therefore, provides an immediate benefit to the public.

The data in Example 18 and the first Grimaldi Declaration are therefore sufficient to establish the asserted utility, and the Examiner has not rebutted the presumption of utility that the Appellants’ application is afforded. Mr. Grimaldi is an expert in the field who conducted or supervised the experiments at issue. His declaration is based on personal knowledge of the relevant facts at issue. Appellants’ have reminded the Examiner that “Office personnel must accept an opinion from a qualified expert that is based upon relevant facts whose accuracy is not being questioned.” *M.P.E.P.* § 2107 (emphasis added). In addition, declarations relating to issues of fact should not be summarily dismissed as “opinions” without an adequate explanation of how the declaration fails to rebut the Examiner’s position. *See in re Alton* 76 F.3d 1168 (Fed. Cir. 1996). The Examiner has offered no reason or evidence to reject either the underlying data or Mr. Grimaldi’s conclusions. Therefore, the Examiner should accept Mr. Grimaldi’s opinion with regard to his statement that “any visually detectable difference seen between two samples is indicative of at least a two-fold difference in cDNA between the tumor tissue and the counterpart normal tissue” and that the genes of interest “can be used to differentiate tumor from normal.”

In conclusion, Appellants submit that the evidence reported in Example 18, supported by the first Grimaldi Declaration, establish that there is at least a two-fold difference in PRO1277 mRNA between esophageal and melanoma tumor tissue and normal esophageal and skin tissue, respectively. Therefore, it follows that the PRO1277 gene, polypeptide, and antibody can be used to distinguish esophageal and melanoma tumor tissue from their normal tissue counterparts. The Examiner has not offered any significant arguments or evidence to the contrary, and

therefore has not established a *prima facie* case that one of skill in the art would reasonably doubt the asserted utility.

b. The two references cited by the Examiner do not refute Appellants' assertion that a change in mRNA levels leads to a corresponding change in the level of the encoded protein

Appellants turn next to Examiner's second argument that "polypeptide levels cannot be accurately predicted from mRNA levels." *Office Action* at 4, 14, and 16. For support, the Examiner cites two references, Haynes *et al.* (Electrophoresis, (1998) 19(11):1862-71) and Chen *et al.* (Mol. and Cell. Proteomics, (2002) 1:304-313). Based on these references, the Examiner concludes that "it is clear that one skilled in the art would not assume that a higher expression of mRNA would correlate with increased polypeptide levels." *Office Action* at 5. For the reasons discussed below, neither of these references are contrary to Appellants' assertion that generally speaking, changes in mRNA levels lead to corresponding changes in the level of polypeptide.

Haynes studied whether there is a correlation between the level of mRNA expression and the level of protein expression for 80 selected genes from yeast. The genes were selected because they constituted a relatively homogeneous group with respect to predicted half-life and expression level of the protein products. *See* Haynes at 1863. Haynes did not examine whether a change in transcript level for a particular gene led to a change in the level of expression of the corresponding protein. Instead, Haynes determined whether the steady-state transcript level correlated with the steady-state level of the corresponding protein based on an analysis of 80 different genes.

Haynes reported to have "found a general trend but no strong correlation between protein and transcript levels." *Id.* However, a cursory inspection of Fig. 1 shows a clear correlation between the mRNA levels and protein levels measured. This correlation is confirmed by an inspection of the full-length research paper from which the data in Fig. 1 were derived, (Gygi *et al.*, Molecular and Cellular Biology, Mar. 1999, 1720-1730), submitted as Exhibit 5 with Appellants' Amendment and Response to Final Office Action. Gygi states that "there was a general trend of increased protein levels resulting from increased mRNA levels," with a correlation coefficient of 0.935, indicating a strong correlation. Gygi at 1726. Moreover, Gygi also states that the correlation is especially strong for highly expressed mRNAs. *Id.* Thus, it is

not clear that Haynes even supports the Examiner's position, as Haynes did report a general trend, and Gygi reports a strong correlation between increasing mRNA levels and increasing protein levels.

The PTO focuses on the portion of Haynes where the authors reported that for some of the studied genes with equivalent mRNA levels, there were differences in corresponding protein expression, including some that varied by more than 50-fold. Similarly, Haynes reports that different proteins with similar expression levels were maintained by transcript levels that varied by as much as 40-fold. *Office Action* at 4-5. Thus, Haynes showed that for one type of yeast, similar mRNA levels for different genes did not universally result in equivalent protein levels for the different gene products, and similar protein levels for different gene products did not universally result from equivalent mRNA levels for the different genes. These results are expected, since there are many factors that determine translation efficiency for a given transcript, or the half-life of the encoded protein. Not surprisingly, based on these results, Haynes concluded that protein levels cannot always be accurately predicted from the level of the corresponding mRNA transcript when looking at the level of transcripts across different genes.

Importantly, Haynes did not say that for a single gene, the level of mRNA transcript is not positively correlated with the level of protein expression. Appellants have asserted that increasing or decreasing the level of mRNA for the same gene leads to a increase or decrease for the corresponding protein. Haynes did not study this issue and says absolutely nothing about it. One cannot look at the level of mRNA across several different genes to investigate whether a change in the level of mRNA a particular gene leads to a change in the level of protein for that gene. Therefore, Haynes is not inconsistent with or contradictory to the utility of the instant claims, and offers no support for the Examiner's rejection of Appellants' asserted utility.

Appellants turn next to the Chen *et al.* reference, where the authors examined the relationship between mRNA levels and protein levels in 76 lung adenocarcinomas and nine non-tumor lung samples.

As an initial matter, it is important to note that a portion of Chen is clearly not relevant to Appellants' assertion that changes in the level of mRNA lead to changes in the level of the encoded polypeptide. In one experiment which was similar to that of Haynes, Chen examined the global relationship between mRNA and the corresponding protein abundance by calculating the average mRNA and protein level of all the samples for each gene or protein, and then looked

for a correlation across different genes. Based on these data, Chen reported that “no significant correlation between mRNA and protein expression was found ($r = -0.025$) if the average levels of mRNA or protein among all samples were applied across the 165 protein spots (98 genes).” *Chen* at Abstract. This measurement of a correlation across different genes is not relevant to Appellants’ asserted utility for the same reasons discussed above with respect to the Haynes *et al.* reference, and is apparently not relied on by the Examiner.

Chen also looked at the level of mRNA of 98 individual genes and their corresponding proteins across the samples. Chen reports that 17% (28 of 165) of the protein spots, or 21.4% (21 of 98) of the genes, showed a statistically significant correlation between protein and mRNA expression. *Chen* at Abstract. It is these results that the Examiner relies on for support.

However, read in its entirety, Chen provides scant evidence to counter Appellants’ asserted utility because portions of Chen support Appellants’ assertions, and the remaining portions provide little insight into the relationship between changes in mRNA levels and changes in the corresponding protein levels for mRNA that is differentially expressed in tumor cells relative to normal cells.

Appellants have asserted that changes in mRNA levels, particularly those which are two-fold or greater, will correspond with measurable changes in polypeptide expression. The data in Chen support Appellants’ assertion. In Figures 2A-2C, Chen plots mRNA value vs. protein value for three genes. In these figures, a wide range of mRNA expression levels were observed (approximately seven- to eight-fold), and a correlation between mRNA and protein levels was observed for all three mRNA/protein pairs. This supports Appellants’ assertion that there is a correlation between changes in mRNA levels which are two-fold or greater and changes in polypeptide expression.

The Examiner relies on the fact that Chen also reports a lack of correlation for some mRNA/protein pairs to support his assertion that polypeptide levels cannot be accurately predicted from mRNA levels. However, as is explained below, the apparent lack of a correlation cannot be used as evidence that Appellants’ assertion of a general correlation is wrong.

To determine if there is a correlation between changes in mRNA and changes in protein levels, one would have to conduct experiments where a measurable change in mRNA for a particular gene is observed, and then examine if there was a corresponding change in the level of the corresponding protein. Stated differently, if there is no substantial change in mRNA levels

for a particular gene, one cannot measure a correlation between changes in mRNA and changes in the encoded protein for that gene. Therefore, one must know if the individual genes studied by Chen were differentially expressed to know if the observed lack of correlation has any relevance to Appellants' assertions of a general correlation between changes in mRNA and protein.

Importantly, unlike Appellants, Chen did not examine differences in mRNA between tumor and normal tissue where one would expect to find substantial changes in the level of mRNA for certain genes. Instead, Chen merely selected proteins whose identity could be determined regardless of any changes in expression level. *Chen* at 306, right column. Therefore, it is not known if there was any substantial difference in mRNA levels for the various studied genes across samples – in short, with the exception of the genes in Figures 2A-2C, it is not known if the genes examined were differentially expressed. Also of significance for Appellants' asserted utility is the fact that Chen did not attempt to examine any differential expression between the cancerous lung samples and the non-cancerous lung samples – Chen did not distinguish between cancer and normal samples in their analysis. Since almost all samples tested by Chen were from the same type of tissue, one would expect most genes examined by Chen to have similar mRNA or protein levels across the samples. In the absence of substantial differential expression, no correlation would be observed. Because it is not known if there was a change in the level of the genes studied by Chen, *i.e.* whether they were differentially expressed, the lack of an observed correlation cannot be used to counter Appellants' assertion.

In sum, the only data reported by Chen which shows substantial changes in the expression of mRNA, Figures 2A-C, confirms Appellants' assertion that substantial changes in mRNA levels (e.g., 2-fold or greater) will correspond to substantial changes in polypeptide expression. Further, these data explain the lack of observed correlation between mRNA levels and protein levels for other genes reported by Chen – there is no indication the genes are differentially expressed. Thus, Chen's results do not refute Appellants' position. Instead, Chen supports Appellants' position that a significant correlation between changes in mRNA and protein levels exists for changes in mRNA levels that are 2-fold or greater.

In further support of Appellants' position, Chen cites Celis *et al.* (FEBS Lett., 480:2-16 (2000)) stating that the authors "found a good correlation between transcript and protein levels among 40 well resolved, abundant proteins using a proteomic and microarray study of bladder

cancer.” *Chen* at 311, first column (emphasis added). As mentioned above, the lack of a correlation across genes is not relevant to Appellants’ asserted utility, and therefore Chen’s discussion of this issue and citation of Anderson and Seilhamer (Electrophoresis, 18:533-37 (1997)) and Gygi *et al.* (Mol. Cell. Bio., 19:1720-30 (1999)) offer no support for the Examiner’s position.

Given the fact that portions of Chen as well as the relevant references cited by Chen support Appellants’ position, and the remainder of Chen cannot be relied on as contrary to the Appellants’ position, the Examiner has failed to establish a *prima facie* case that one of skill in the art would doubt Appellants’ asserted utility based on any lack of correlation between changes in mRNA level and changes in the corresponding protein level.

c. **Conclusion – Examiner has failed to establish a prima facie case that one of skill in the art would doubt Appellants’ asserted utility**

The Examiner has relied on essentially two arguments in rejecting the pending claims for lack of utility. First, the Examiner has questioned the sufficiency, reliability and significance of the data reported in Example 18 as well as the supporting first Grimaldi declaration. The Examiner has argued that absent some known translocation or mutation of PRO1277, or some role for PRO1277 in cancer formation or development, the disclosure is insufficient. Second, the Examiner relies on Haynes *et al.* and Chen *et al.* to support the assertion that polypeptide levels cannot be accurately predicted from mRNA levels. Appellants have responded to each of these arguments in turn.

First, Appellants have shown that the data in Example 18 are sufficient to show that PRO1277 is useful as a cancer diagnostic tool. This assertion is supported by the first Grimaldi declaration. The Examiner has not provided any substantial reason or evidence for one of skill in the art to doubt the reliability or usefulness of Example 18, or the facts and conclusions in the first Grimaldi declaration.

Second, Appellants have shown the Haynes references is simply not relevant to the issue of whether a change in mRNA levels leads to a corresponding change in the level of the encoded protein. Appellants have also shown that portions of Chen *et al.*, as well as some of the references cited by Chen, actually support Appellants assertion that changes in mRNA levels

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generally correlate with changes in the level of the encoded polypeptide. The remainder of Chen is not reliable enough to offer any support for the Examiner's position.

Taken together, the Examiner's arguments are not sufficient to satisfy the Examiner's burden to "provide[] evidence showing that one of ordinary skill in the art would reasonably doubt the asserted utility." *In re Brana*, 51 F.3d 1560, 1566, 34 U.S.P.Q.2d 1436 (Fed. Cir. 1995). The Examiner's arguments are largely conclusory statements which are not supported by any substantial evidence or reasoning which explains why one of ordinary skill in the art would reasonably doubt the asserted utility. Therefore, the Board should accept the Appellants' disclosure of utility. *See Ex parte Rubin*, 5 U.S.P.Q. 2d 1461 (Bd. Pat. App. & Interf. 1987) ("There is no factual support in this record for the examiner's questioning of the denaturation test reported in the specification. ... No reason to doubt 'the objective truth' of the asserted utility having been advanced by the examiner, we accept appellant's disclosure of utility corresponding in scope to the claimed subject matter.").

8. Appellants have provided Sufficient Rebuttal Evidence of Utility

"Only after the PTO provides evidence showing that one of ordinary skill in the art would reasonably doubt the asserted utility does the burden shift to the applicant to provide rebuttal evidence." *In re Brana*, 51 F.3d 1560, 1566, 34 U.S.P.Q.2d 1436 (Fed. Cir. 1995). The rebuttal evidence must be sufficient such that when it is considered as a whole, it is more likely than not that the asserted utility is true. *See In re Oetiker*, 977 F.2d 1443, 1445, 24 U.S.P.Q.2d 1443, 1444 (Fed. Cir. 1992) (stating that the evidentiary standard to be used throughout *ex parte* examination in setting forth a rejection is a preponderance of the evidence, or "more likely than not" standard). The M.P.E.P. summarizes the standard of proof required:

[T]he applicant does not have to provide evidence sufficient to establish that an asserted utility is true "beyond a reasonable doubt." Nor must the applicant provide evidence such that it establishes an asserted utility as a matter of statistical certainty. Instead, evidence will be sufficient if, considered as a whole, it leads a person of ordinary skill in the art to conclude that the asserted utility is more likely than not true. *M.P.E.P.* § 2107.02, part VII (emphasis in original, citations omitted).

Appellants remind the Board that the Federal Circuit has stated that the standard for satisfying the utility requirement is a low one: "The threshold of utility is not high: An invention is 'useful'

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under section 101 if it is capable of providing some identifiable benefit.” *Juicy Whip, Inc. v. Orange Bang, Inc.*, 185 F.3d 1364, 1366, 51 U.S.P.Q. 2d 1700 (Fed. Cir. 1999).

Even if the Examiner has satisfied his burden of presenting a *prima facie* case of lack of utility, Appellants have supplied more than enough rebuttal evidence, such that when considered as a whole, one of skill in the art would conclude that the asserted utility is more likely than not true. As discussed in detail below, Appellants have provided sufficient evidence that the gene encoding the PRO1277 polypeptide is differentially expressed in certain cancers and can therefore be used as a diagnostic tool. In addition, Appellants have shown that it is well established in the art that there is a reasonable correlation between changes in mRNA level and changes in the corresponding protein level such that one of skill in the art would believe that the PRO1277 polypeptide is also differentially expressed in certain cancers. Therefore, considering the evidence as a whole, one of skill in the art would believe that it is more likely than not that the claimed antibodies are useful as diagnostic tools for cancer, particularly esophageal and melanoma tumors.

a. Appellants have established that the gene encoding the PRO1277 polypeptide is differentially expressed in certain cancers

As discussed above, the Examiner has not provided any evidence or reasoning to challenge the reliability and significance of the data in Example 18 which reports that the mRNA for PRO1277 is more highly expressed in normal esophageal and skin tissue compared to esophageal and melanoma tumor, respectively. In contrast to this complete lack of evidence on the part of the Examiner, Appellants have submitted the first Grimaldi declaration. That declaration establishes that it is the opinion of an expert in the field who has personal knowledge of the facts surrounding Example 18 that there is at least a two-fold difference in mRNA for PRO1277 between the tumor tissue and the counterpart normal tissue, and that the PRO1277 genes, polypeptides and antibodies are useful for differentiating tumor tissue from normal tissue. The Examiner has not provided any evidence or reasoning to challenge the facts and conclusions of the first Grimaldi declaration in support of Example 18.

Given the disclosure of Example 18 and the supporting first Grimaldi declaration on the one hand, and the complete lack of any evidence on the other, it is clear that considering the evidence as a whole, one of skill in the art would conclude that it is more likely than not that the

PRO1277 gene is differentially expressed in esophageal and melanoma tumor tissue compared to their normal tissue counterparts such that is useful as a diagnostic tool to distinguish tumor tissue from normal tissue.

As Appellants explain below, it is more likely than not that the PRO1277 polypeptide is also differentially expressed in esophageal and melanoma tumor tissue, and can therefore be used to distinguish tumor tissue from normal tissue. This provides utility for the claimed antibodies to the PRO1277 polypeptide.

b. Appellants have established that generally there is a correlation between changes in mRNA expression levels and changes in the expression level of the encoded protein

Appellants next turn to the second portion of their argument in support of their asserted utility – that it is well-established in the art that in most cases a change in the level of mRNA for a particular protein leads to a corresponding change in the level of the encoded protein. Given Appellants’ evidence of differential expression of the mRNA for the PRO1277 polypeptide in esophageal and melanoma tumor, it is more likely than not that the PRO1277 polypeptide is likewise differentially expressed, and therefore the claimed antibodies are useful as diagnostic tools, particularly for esophageal and melanoma tumor.

In support of the assertion that changes in mRNA are positively correlated to changes in protein levels, Appellants submitted a second Declaration by J. Christopher Grimaldi, an expert in the field of cancer biology (originally submitted as Exhibit 6 with the Appellants’ Amendment and Response to Office Action). As stated in paragraph 5 of the declaration, “Those who work in this field are well aware that in the vast majority of cases, when a gene is over-expressed...the gene product or polypeptide will also be over-expressed.... This same principal applies to gene under-expression.” *Second Grimaldi Declaration* at ¶ 5. Further, “increased mRNA expression is expected to result in increased polypeptide expression, and the detection of decreased mRNA expression is expected to result in decreased polypeptide expression.” *Id.*

Appellants also submitted the declaration of Paul Polakis, Ph.D. an expert in the field of cancer biology (attached as Exhibit 7 to Appellants’ Amendment and Response to Office Action). As stated in paragraph 6 of his declaration:

Based on my own experience accumulated in more than 20 years of research, including the data discussed in paragraphs 4 and 5 above [showing a positive

correlation between mRNA levels and encoded protein levels in the vast majority of cases studied in relation to the present invention] and my knowledge of the relevant scientific literature, it is my considered scientific opinion that for human genes, an increased level of mRNA in a tumor cell relative to a normal cell typically correlates to a similar increase in abundance of the encoded protein in the tumor cell relative to the normal cell. In fact, it remains a central dogma in molecular biology that increased mRNA levels are predictive of corresponding increased levels of the encoded protein. *Polakis Declaration* at ¶ 6 (emphasis added).

Dr. Polakis acknowledges that there are published cases where such a correlation does not exist, but states that it is his opinion, based on over 20 years of scientific research, that “such reports are exceptions to the commonly understood general rule that increased mRNA levels are predictive of corresponding increased levels of the encoded protein.” *Polakis Declaration* at ¶ 6.

The statements of Grimaldi and Polakis are supported by the teachings in *Molecular Biology of the Cell*, a leading textbook in the field (Bruce Alberts, *et al.*, *Molecular Biology of the Cell* (3rd ed. 1994) (submitted with Appellants’ Amendment and Response to Final Office Action as Exhibit 6, hereinafter “Cell 3rd”) and (4th ed. 2002) (submitted with Appellants’ Amendment and Response to Final Office Action as Exhibit 7, hereinafter “Cell 4th”). Figure 9-2 of Cell 3rd shows the steps at which eukaryotic gene expression can be controlled. The first step depicted is transcriptional control. Cell 3rd provides that “[f]or most genes transcriptional controls are paramount. This makes sense because, of all the possible control points illustrated in Figure 9-2, only transcriptional control ensures that no superfluous intermediates are synthesized.” *Cell 3rd* at 403 (emphasis added). In addition, the text states that “Although controls on the initiation of gene transcription are the predominant form of regulation for most genes, other controls can act later in the pathway from RNA to protein to modulate the amount of gene product that is made.” *Cell 3rd* at 453 (emphasis added). Thus, as established in Cell 3rd, the predominant mechanism for regulating the amount of protein produced is by regulating transcription.

In Cell 4th, Figure 6-3 on page 302 illustrates the basic principle that there is a correlation between increased gene expression and increased protein expression. The accompanying text states that “a cell can change (or regulate) the expression of each of its genes according to the needs of the moment – *most obviously by controlling the production of its mRNA.*” *Cell 4th* at 302 (emphasis added). Similarly, Figure 6-90 on page 364 of Cell 4th illustrates the path from gene to protein. The accompanying text states that while potentially each step can be regulated

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by the cell, “the initiation of transcription is the most common point for a cell to regulate the expression of each of its genes.” *Cell 4th* at 364 (emphasis added). This point is repeated on page 379, where the authors state that of all the possible points for regulating protein expression, “[f]or most genes transcriptional controls are paramount.” *Cell 4th* at 379 (emphasis added).

Further support for Appellants’ position can be found in the textbook, *Genes VI*, (Benjamin Lewin, *Genes VI* (1997)) (submitted with Appellants’ After Final Amendment as Exhibit 8) which states “having acknowledged that control of gene expression can occur at multiple stages, and that production of RNA cannot inevitably be equated with production of protein, it is clear that the overwhelming majority of regulatory events occur at the initiation of transcription.” *Genes VI* at 847-848 (emphasis added).

Additional support is also found in Zhigang *et al.*, *World Journal of Surgical Oncology* 2:13, 2004 (submitted with Appellants’ Amendment and Response to Final Office Action as Exhibit 9). Zhigang studied the expression of prostate stem cell antigen (PSCA) protein and mRNA to validate it as a potential molecular target for diagnosis and treatment of human prostate cancer. The data showed “a high degree of correlation between PSCA protein and mRNA expression” *Zhigang* at 4. Of the samples tested, 81 out of 87 showed a high degree of correlation between mRNA expression and protein expression. The authors conclude that “it is demonstrated that PSCA protein and mRNA overexpressed in human prostate cancer, and that the increased protein level of PSCA was resulted from the upregulated transcription of its mRNA.” *Id.* at 6. Even though the correlation between mRNA expression and protein expression occurred in 93% of the samples tested, not 100%, the authors state that “PSCA may be a promising molecular marker for the clinical prognosis of human Pca and a valuable target for diagnosis and therapy of this tumor.” *Id.* at 7.

Further, Meric *et al.*, *Molecular Cancer Therapeutics*, vol. 1, 971-979 (2002), (submitted with Appellants’ Amendment and Response to Final Office Action as Exhibit 10), states the following:

The **fundamental principle** of molecular therapeutics in cancer is to exploit the differences in gene expression between cancer cells and normal cells...[M]ost efforts have concentrated on identifying differences in gene expression at the level of mRNA, which can be attributable to either DNA amplification or to differences in transcription. *Meric et al.* at 971 (emphasis added).

Exploiting differences in gene expression between cancer cells and normal cells would not be a “fundamental principle” of molecular cancer therapeutics if there were no significant correlation between gene expression and protein levels. Stated another way, changes in mRNA without corresponding changes in protein levels would have little or no effect on cellular biology, and those of skill in the art would have no reason to examine the differences in gene expression at the mRNA level without such a correlation. However, as one of skill in the art recognizes, there is a strong correlation between changes in mRNA and changes in protein level. It is because of this strong correlation that it remains a “fundamental principle” of molecular therapeutics in cancer to look at changes in mRNA level.

Together, the declarations of Grimaldi and Polakis, the accompanying references, and the excerpts and references discussed above all establish that the accepted understanding in the art is that there is a reasonable correlation between changes in gene expression and changes in the level of the encoded protein. In contrast to this substantial amount of evidence supporting Appellants’ position, the Examiner has cited two references, Haynes *et al.* and Chen *et al.* However, as discussed above, Haynes is not relevant to the issue of whether a change in mRNA levels leads to a change in the level of the corresponding protein. Likewise, portions of Chen and the relevant references cited by Chen actually support Appellants’ position, and the remainder of Chen is inconclusive. It is clear that when considered as a whole, the preponderance of the evidence clearly weighs in favor of Appellants.

Appellants have presented sufficient evidence to establish that the mRNA for PRO1277 is differentially expressed in esophageal and melanoma tumors compared to their normal tissue counterparts, and that it is more likely than not that this leads to differential expression of the PRO1277 polypeptide. This makes the claimed antibodies to PRO1277 polypeptide useful for diagnosing cancer, particularly esophageal and melanoma tumors. Given the overwhelming amount of evidence in support of Appellants’ position, and the near absence of any evidence in support of the Examiner’s position, when considered as a whole the evidence leads a person of ordinary skill in the art to conclude that the asserted utility is more likely than not true.

c. **The asserted utility is specific**

Finally, Appellants address the PTO’s assertion that the asserted utilities are not specific to the claimed antibodies related to PRO1277.

Specific Utility is defined as utility which is “specific to the subject matter claimed,” in contrast to “a general utility that would be applicable to the broad class of the invention.” *M.P.E.P.* § 2107.01 I. Appellants submit that the evidence of differential expression of the PRO1277 gene and polypeptide in certain types of tumor cells, along with the declarations and references discussed above, provide a specific utility for the claimed antibodies.

As discussed above, there are significant data which show that the gene for the PRO1277 polypeptide is expressed at least two-fold higher in normal esophageal and skin tissue compared to esophageal and melanoma tumor, respectively. These data are strong evidence that the PRO1277 gene and polypeptide are associated with esophageal and melanoma tumors. Thus, contrary to the assertions of the Examiner, Appellants have provided evidence associating the PRO1277 gene and polypeptide with a specific disease. The asserted utility for antibodies to the PRO1277 polypeptide as a diagnostic tool for cancer, particularly esophageal and melanoma tumor, is a specific utility – it is not a general utility that would apply to the broad class of antibodies.

9. ***The Examiner’s Response to Appellants’ Evidence is Insufficient to Rebut Appellants’ Arguments***

The Examiner has stated that the Grimaldi and Polakis declarations are “insufficient to overcome the rejection of claims 1-5” based on 35 U.S.C. §§ 101 and 112. *Office Action* at 6.

a. ***The Examiner’s response to the First Grimaldi Declaration***

The Examiner has rejected the first Grimaldi Declaration based on two arguments. The first argument is that “there is no evidentiary art that would corroborate for example, that ‘any visually detectable difference seen between two samples is indicative of at least a two-fold difference in cDNA between the tumor tissue and the counterpart normal tissue.’” *Office Action* at 13 (quoting first Grimaldi Declaration).

Appellants submit that the declaration of Mr. Grimaldi is based on personal knowledge of the relevant facts at issue. Mr. Grimaldi is an expert in the field and conducted or supervised the experiments at issue. Appellants have reminded the Examiner that “[o]ffice personnel must accept an opinion from a qualified expert that is based upon relevant facts whose accuracy is not being questioned.” PTO Utility Examination Guidelines (2001) (emphasis added). In addition,

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declarations relating to issues of fact should not be summarily dismissed as “opinions” without an adequate explanation of how the declaration fails to rebut the Examiner’s position. *In re Alton* 76 F.3d 1168 (Fed. Cir. 1996).

In addition, Appellants provided as Exhibit 1 to their Amendment and Response to Final Office Action a copy of page 122 of the 2002-2003 New England Biolabs catalog. This exhibit shows DNA size markers of differing lengths run on an agarose gel. The column on the left provides the mass of each marker in nanograms and the column on the right provides the length of the marker. It is apparent that the band intensity of markers having mass differences of two-fold are readily distinguishable by eye (*see, e.g.*, the difference in band intensities of the 0.1kb fragment present at 61ng and the 0.5kb marker present at 124ng). Accordingly, Appellants maintain that the procedures used to detect differences in expression levels were sufficiently sensitive to detect two-fold differences.

The Examiner has not supplied any reasons or evidence to question the accuracy of the facts upon which Mr. Grimaldi based his opinions. Mr. Grimaldi has personal knowledge of the relevant facts, has based his opinion on those facts, and the Examiner has offered no reason or evidence to reject either the underlying facts or his opinion. Therefore, the Examiner and Board should accept Mr. Grimaldi’s opinion with regard to his statement that “any visually detectable difference seen between two samples is indicative of at least a two-fold difference in cDNA between the tumor tissue and the counterpart normal tissue” and that the nucleic acids of interest “can be used to differentiate tumor from normal.” Together, these statements establish that there is at least a two-fold difference in expression, and that the results are reliable enough that they can be used to distinguish tumor from normal tissue.

The Examiner’s second argument in response to the first Grimaldi declaration is that “one cannot determine from the data in the specification whether the observed ‘amplification’ of nucleic acid is due to increase in copy number, or alternatively due to increase in transcription rates,” and that the specification does not provide any information regarding “differential mRNA levels of PRO1277,” but rather “describes only gene amplification data.” *Office Action* at 12.

Appellants again emphasize that the data in Example 18 are gene expression data, not gene amplification data. The specification and the first Grimaldi Declaration make clear that Example 18 used semi-quantitative PCR of cDNA libraries. Therefore, one of skill in the art would know that Example 18 is a measure of mRNA levels, and reflects differential PRO1277

gene expression, not gene amplification. Therefore, the Examiner's arguments regarding gene amplification do not support the Examiner's challenge of the sufficiency of the Example 18 data, or the first Grimaldi Declaration.

b. The Examiner's response to the Second Grimaldi Declaration

In response to the second Grimaldi Declaration, the Examiner focuses on paragraph 4 of the declaration where it states that for chromosomal aberrations which result in aberrant expression of a mRNA and corresponding protein, "the gene product is a promising target for cancer therapy, for example, by the therapeutic antibody approach." *Office Action* at 8 (emphasis added). The Examiner rejects this argument, stating that it was not persuasive because unlike the genes discussed in the references cited in the declaration, "[t]he PRO1277 gene, ... has *not* been associated with tumor formation or the development of cancer, nor has it been shown to be predictive of such. Similarly, ... no translocation of PRO1277 is known to occur. ... No mutation or translocation of PRO1277 has been associated with esophagus or skin cancer." *Office Action* at 8-9. The Examiner concluded that "[i]n the absence of any of the above information" the disclosure was insufficient to satisfy the requirements of § 101. *Id.* at 9.

The Examiner's arguments fail to establish that one of skill in the art would doubt Appellants' asserted utility. Once again, the Examiner has failed to establish how the "absence of any of the above information" is relevant to the asserted utility by supplying evidence or reasoning to support his assertion. *See In re Brana*, 51 F.3d 1560, 1566, 34 U.S.P.Q.2d 1436 (Fed. Cir. 1995) ("Only after the PTO provides evidence showing that one of ordinary skill in the art would reasonably doubt the asserted utility does the burden shift to the Appellant to provide rebuttal evidence.") (emphasis added).

The lack of a known role for PRO1277 in tumor formation or the development of cancer does not prevent its use as a diagnostic tool for cancer. Likewise, the fact that there is no known translocation or mutation of PRO1277 is irrelevant to whether its differential expression can be used to assist in diagnosis of cancer – one does not need to know why PRO1277 is differentially expressed, or what the consequence of the differential expression is, in order to exploit the differential expression to distinguish tumor from normal tissue.

The Revised Interim Utility Guidelines promulgated by the PTO recognize that proteins which are differentially expressed in cancer have utility. (See the caveat in Example 12 which

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state that the utility requirement is satisfied where a protein is expressed in melanoma cells but not on normal skin and antibodies against the protein can be used to diagnose cancer.) In addition, while Appellants appreciate that actions taken in other applications are not binding on the PTO with respect to the present application, Appellants note that the PTO has issued several patents claiming differentially expressed polypeptides and antibodies to the same, or methods employing such antibodies. *See, e.g.*, U.S. Patent No. 6,414,117, U.S. Patent No. 6,124,433, U.S. Patent No. 6,156,500, and U.S. Patent No. 6,562,343.

In addition, Appellants note that they did not even rely on the portion of the second Grimaldi declaration cited by the Examiner which discusses targets for cancer therapy. Instead, Appellants submitted the second Grimaldi declaration in support of the assertion that changes in mRNA are positively correlated to changes in protein levels. Appellants relied on paragraph 5 of the declaration which states: "Those who work in this field are well aware that in the vast majority of cases, when a gene is over-expressed...the gene product or polypeptide will also be over-expressed.... This same principal applies to gene under-expression." *Amendment and Response to Final Office Action* at 21, quoting *Second Grimaldi Declaration* at ¶ 5. As support for this statement, Mr. Grimaldi noted that "[t]echniques used to detect mRNA, such as Northern Blotting, Differential Display, *in situ* hybridization, quantitative PCR, Taqman, and more recently Microarray technology all rely on the dogma that a change in mRNA will represent a similar change in protein. If this dogma did not hold true then these techniques would have little value and not be so widely used." *Second Grimaldi Declaration* at ¶ 5. Whether the differential expression of mRNA is due to mutations or translocations has no bearing on the portion of the Grimaldi reference relied on by Appellants.

c. The Examiner's response to the Polakis Declaration

In response to the Polakis Declaration, the Examiner makes two arguments. First, the Examiner states that only Dr. Polakis' conclusions are provided in the declaration. This is clearly not the case.

Appellants rely on the following portion of the Polakis Declaration:

Based on my own experience accumulated in more than 20 years of research, including the data discussed in paragraphs 4 and 5 above and my knowledge of the relevant scientific literature, it is my considered scientific opinion that for human genes, an increased level of mRNA in a tumor cell relative to a normal cell typically correlates to a similar increase in abundance of the encoded protein in

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the tumor cell relative to the normal cell. In fact, it remains a central dogma in molecular biology that increased mRNA levels are predictive of corresponding increased levels of the encoded protein. *Polakis Declaration* at ¶ 6 (emphasis added).

Paragraphs 4 and 5 of the Polakis Declaration disclose that in the course of his research which is closely related to the instant invention, Dr. Polakis has identified approximately 200 gene transcripts that are differentially expressed in human tumors. He has generated antibodies to about 30 of the protein products. In paragraph 5, he states that:

[T]here is a strong correlation between changes in the level of mRNA present in any particular cell type and the level of protein expressed from that mRNA in that cell type. In approximately 80% of our observations we have found that increases in the level of a particular mRNA correlates with changes in the level of protein expressed from that mRNA when human tumor cells are compared with their corresponding normal cells. *Polakis Declaration* at ¶ 5.

Clearly, paragraphs 4 and 5 provide significant evidentiary support for his conclusions in paragraph 6. As to his statement that it is a central dogma of molecular biology that increases in mRNA lead to increases in protein, this statement is also supported by the data in paragraphs 4 and 5, as well as Dr. Polakis' expertise and more than 20 years of research in the field. Appellants remind the Board that "[o]ffice personnel must accept an opinion from a qualified expert that is based upon relevant facts whose accuracy is not being questioned." PTO Utility Examination Guidelines (2001) (emphasis added). In addition, declarations relating to issues of fact should not be summarily dismissed as "opinions" without an adequate explanation of how the declaration fails to rebut the Examiner's position. *In re Alton* 76 F.3d 1168 (Fed. Cir. 1996).

The Examiner's second response to the Polakis declaration that there is a correlation between changes in the level of mRNA and changes in the level of the encoded protein is that:

[I]t is important to note that the instant specification provides no information regarding differential mRNA levels of PRO1277 in tumor samples as contrasted to normal tissue samples or the corresponding protein levels. Only gene amplification data were presented. Therefore the declaration is insufficient to overcome the [utility and enablement] rejection of claims 1-5...since it is limited to a discussion of data regarding the correlation of mRNA levels and polypeptide levels. *Office Action* at 13-14.

As discussed above, this assertion is simply wrong. The data in Example 18 are differential mRNA data regarding the level of PRO1277 mRNA in tumor samples compared to normal tissue samples.

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Appellants also address the Examiner's statement that further research is required for the invention, and that this requirement "is borne out by Grimaldi assertion that 'additional studies can then be conducted if further information is desired.'" *Office Action* at 13

The Examiner's reliance on the quote from the first Grimaldi declaration is clearly misplaced when read in context:

7. The results of the gene expression studies indicate that the genes of interest can be used to differentiate tumor from normal. The precise levels of gene expression are irrelevant; what matters is that there is a relative difference in expression between normal tissue and tumor tissue. ...**If a difference is detected, this indicates that the gene and its corresponding polypeptide and antibodies against the polypeptide are useful for diagnostic purposes, to screen samples to differentiate between normal and tumor.** Additional studies can then be conducted if further information is desired. *First Grimaldi Declaration* at ¶ 7 (emphasis added).

It is obvious that Mr. Grimaldi was stating that it is his expert opinion that the information provided in Example 18 is sufficient to use the gene, protein and antibody as diagnostic tools, and that no further testing or information is required. However, if additional information is desired, such as the role of the gene or protein in cancer formation or growth, additional studies can be conducted. It is disingenuous of the Examiner to take this quote out of context to suggest that Mr. Grimaldi is stating that further research is required to use the claimed invention when the remainder of his declaration clearly states otherwise.

Finally, the Examiner concludes his arguments by stating that "even if there were a correlation between mRNA levels and protein levels, Applicants have not established a nexus between the cDNA of instant invention and PRO1277 protein....Whether or not increased levels of PRO1277 mRNA correlates with increased levels of PRO1277 protein is not an issue." *Office Action* at 17.

There is an obvious nexus between the PRO1277 cDNA and the PRO1277 polypeptide. First, as explained above, cDNA is made from mRNA, and thus the changes in PRO1277 cDNA reported in Example 18 reflect changes in PRO1277 mRNA. Second, as described in numerous references and declarations above, regulation of mRNA is the primary method for controlling the expression of a gene, and there is a general correlation between changes in mRNA levels and changes in protein levels. Because PRO1277 cDNA and mRNA encodes the PRO1277 polypeptide, changes in PRO1277 mRNA levels lead to changes in PRO1277 polypeptide levels – the nexus between mRNA and the encoded protein is well-established.

In conclusion, none of the Examiner's responses to Appellants' supporting evidence are sufficient to rebut Appellants' asserted utility.

10. *The Courts have held that the Utility Requirement was Satisfied in Similar Cases*

The seminal decision interpreting the utility requirement of 35 U.S.C. § 101 is *Brenner v. Manson*, 383 U.S. 519, 148 U.S.P.Q. 689 (1966). At issue in *Brenner* was a claim to "a chemical process which yields an already known product whose utility – other than as a possible object of scientific inquiry – ha[d] not yet been evidenced." *Id.* at 529, 148 U.S.P.Q. at 693. The Patent Office rejected the claimed process for lack of utility because the product produced by the claimed process had no known use. *See id.* at 521-22, 148 U.S.P.Q. at 690. On appeal, the Court of Customs and Patent Appeals reversed, holding "where a claimed process produces a known product it is not necessary to show utility for the product." *Id.* at 522, 148 U.S.P.Q. at 691.

In reviewing the lower court's decision, the Court made its oft quoted statement that "[t]he basic quid pro quo contemplated by the Constitution and the Congress for granting a patent monopoly is the benefit derived by the public from an invention with substantial utility. Unless and until a process is refined and developed to this point – where specific benefit exists in currently available form – there is insufficient justification for permitting an Appellant to engross what may prove to be a broad field." *Id.* at 534-35, 148 U.S.P.Q. at 695.

The first opinion of the C.C.P.A. applying *Brenner* was *In re Kirk*, 376 F.2d 936, 153 U.S.P.Q. 48 (C.C.P.A. 1967). The invention claimed in *Kirk* was a set of steroid derivatives said to have valuable biological properties and to be of value "in the furtherance of steroidal research and in the application of steroidal materials to veterinary or medical practice." *Id.* at 938, 153 U.S.P.Q. at 50. In affirming the claim rejection based on a lack of utility, the court held that the "nebulous expressions 'biological activity' or 'biological properties'" did not adequately convey how to use the claimed compounds." *Id.* at 941, 153 U.S.P.Q. at 52. The court also rejected Appellants' supporting affidavit, stating, "the sum and substance of the affidavit appears to be that one of ordinary skill in the art would know 'how to use' the compounds to find out in the first instance whether the compounds are – or are not – in fact useful or possess useful properties, and to ascertain what those properties are." *Id.* at 942, 153 U.S.P.Q. at 53.

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Since these early decisions, the courts have continued to clarify what is sufficient to satisfy the utility requirement. Three more recent decisions are of particular relevance to the instant application: *Nelson v. Bowler*, 626 F.2d 853, 206 U.S.P.Q. 881 (C.C.P.A. 1980), *Cross v. Iizuka*, 753 F.2d 1040, 224 U.S.P.Q. 739 (Fed. Cir. 1985), and *Fujikawa v. Wattanasin*, 93 F.3d 1559, 39 U.S.P.Q. 2d 1895 (Fed. Cir. 1996).

The earliest of these cases, *Nelson v. Bowler*, involved an interference between two applications related to derivatives of naturally occurring prostaglandins (PG). *Nelson*, 626 F.2d at 854-55. The issue was whether Nelson had shown at least one utility for the compounds at issue to establish an actual reduction to practice. *Id.* at 855. The Appellants relied on two tests to prove practical utility: an *in vivo* rat blood pressure (BP) test and an *in vitro* gerbil colon smooth muscle stimulation (GC-SMS) test. In the BP test, the blood pressure of anesthetized rats was recorded on a polygraph chart to determine whether an injected compound had any effect. Responses were categorized as either a depressor (lowering) effect or a pressor (elevating) effect. *Id.* In the GC-SMS test a section of colon was excised from a freshly-killed gerbil for suspension in a physiological solution, and a lever arm was connected to the colon in such a way that any contraction was recorded as a polygraph trace. *Id.* The Board held that Nelson had not shown adequate proof of practical utility, characterizing the tests as “rough screens, uncorrelated with actual utility.” *Id.* at 856.

On appeal the C.C.P.A. reversed, holding that the Board “erred in not recognizing that tests evidencing pharmacological activity may manifest a practical utility even though they may not establish a specific therapeutic use.” *Id.* The Court stated that “practical utility” was characterized as a use of the claimed discovery in a manner which provides some immediate benefit to the public, establishing the following rule:

Knowledge of the pharmacological activity of any compound is obviously beneficial to the public. It is inherently faster and easier to combat illnesses and alleviate symptoms when the medical profession is armed with an arsenal of chemicals having known pharmacological activities. Since it is crucial to provide researchers with an incentive to disclose pharmacological activities in as many compounds as possible, we conclude that adequate proof of any such activity constitutes a showing of practical utility. *Id.* (emphasis added).

The Court rejected Bowler’s argument that the BP and GC-SMS tests are inconclusive showings of pharmacological activity since confirmation by statistically significant means did not occur until after the critical date. The Court stated that “a rigorous correlation is not

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necessary where the test for pharmacological activity is reasonably indicative of the desired response.” *Id.* (emphasis added). The Court concluded that a “reasonable correlation” between the observed properties and the suggested use was sufficient to establish practical utility. *Id.* at 857.

The sufficiency of a “reasonable correlation” in establishing utility was affirmed by the Court of Appeals for the Federal Circuit in *Cross v. Iizuka*, 753 F.2d 1040, 224 U.S.P.Q. 739 (Fed. Cir. 1985). In *Cross*, the subject of the interference before the Court was imidazole derivative compounds which inhibit the synthesis of thromboxane synthetase, an enzyme which leads to the formation of thromboxane A₂. At the time the applications were filed, thromboxane A₂ was postulated to be involved in platelet aggregation, which was associated with several deleterious conditions. *Id.* at 1042.

The question before the Board and reviewed by the Court was whether Iizuka was entitled to the benefit of his Japanese priority application. *Id.* The Japanese application disclosed that the imidazole derivatives showed strong inhibitory action for thromboxane synthetase from human or bovine platelet microsomes, an *in vitro* utility. *Id.* at 1043. Relying in part on *Nelson*, the Board held that tests evidencing pharmacological activity may manifest a practical utility even though they may not establish a specific therapeutic use, and concluded that the *in vitro* tests were sufficient to establish a practical utility. *Id.*

On appeal, Cross argued that the basic *in vitro* tests conducted in cellular fractions did not establish a practical utility for the claimed compounds, and that more sophisticated *in vitro* or *in vivo* tests were necessary to establish a practical utility. *Id.* at 1050. The Court rejected this argument, noting that adequate proof of any pharmaceutical activity constitutes a showing of practical utility. *Id.* The Court accepted the argument that initial testing of compounds is widely done *in vitro*:

[I]n *vitro* results...are generally predictive of *in vivo* test results, i.e., there is a reasonable correlation therebetween. Were this not so, the testing procedures of the pharmaceutical industry would not be as they are. Iizuka has not urged, and rightly so, that there is an invariable exact correlation between *in vitro* test results and *in vivo* test results. Rather, Iizuka’s position is that successful *in vitro* testing for a particular pharmacological activity establishes a significant probability that *in vivo* testing for this particular pharmacological activity will be successful. *Id.* (emphasis added).

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The Court also noted that in previous decisions, its predecessor court had accepted evidence of *in vivo* utility as sufficient to establish practical utility. The Court reasoned that:

This *in vivo* testing is but an intermediate link in a screening chain which may eventually lead to the use of the drug as a therapeutic agent in humans. We perceive no insurmountable difficulty, under appropriate circumstances, in finding that the first link in the screening chain, *in vitro* testing, may establish a practical utility for the compound in question. Successful *in vitro* testing will marshal resources and direct the expenditure of effort to further *in vivo* testing of the most potent compounds, thereby providing an immediate benefit to the public, analogous to the benefit provided by the showing of an *in vivo* utility. *Id.* at 1051, citing *Nelson*, 626 F.2d at 856 (emphasis added).

Based on this reasoning, the Court affirmed the decision of the Board, stating that “based upon the relevant evidence as a whole, there is a reasonable correlation between the disclosed *in vitro* utility and an *in vivo* activity, and therefore a rigorous correlation is not necessary where the disclosure of pharmacological activity is reasonable based upon the probative evidence.” *Id.* at 1050 (emphasis added). The Court therefore held that the disclosed *in vitro* utility was “sufficient to comply with the practical utility requirement of § 101.” *Id.* at 1051.

The holdings of *Nelson* and *Cross* were more recently affirmed in *Fujikawa v. Wattanasin*, 93 F.3d 1559, 39 U.S.P.Q.2d 1895 (Fed. Cir. 1996). In *Fujikawa*, the Court again affirmed the notion that initial screens of compounds provide a practical utility even though they may not provide a therapeutic use because “[i]t is inherently faster and easier to combat illnesses and alleviate symptoms when the medical profession is armed with an arsenal of chemicals having known pharmacological activities.” *Id.* at 1564, quoting *Nelson*, 626 F.2d at 856. The Court noted that it may be difficult to predict whether novel compounds will exhibit pharmacological activity, and consequently testing is often required to establish practical utility. *Id.* However the Court went on to state:

But the test results need not absolutely prove that the compound is pharmacologically active. All that is required is that the tests be “*reasonably* indicative of the desired [pharmacological] response.” In other words, there must be a sufficient correlation between the tests and an asserted pharmacological activity so as to convince those skilled in the art, to a reasonable probability, that the novel compound will exhibit the asserted pharmacological behavior.” *Id.* (internal citations omitted, underline emphasis added, italics in original).

On appeal, *Fujikawa* argued that *Wattanasin* had failed to establish an adequate correlation between the *in vitro* and *in vivo* results to permit *Wattanasin* to rely on positive *in*

vitro results to establish a practical utility. The Court stated that the Board relied on testimony from those skilled in the art that the *in vitro* results convinced the experts that the claimed compounds would exhibit the desired pharmacological activity when administered *in vivo*, including testimony that *in vivo* activity is typically highly correlatable to a compound's *in vitro* activity in the field. *Id.* at 1565. To overcome this evidence and counter the Board's decision, Fujikawa pointed to the testimony of its expert that "there is a reasonable element of doubt that some elements may be encountered which are active in the *in vitro* assay, but yet inactive in the *in vivo* assay." *Id.*

The Court rejected this argument: "Of course, it is possible that some compounds active *in vitro* may not be active *in vivo*. But, as our predecessor court in *Nelson* explained, a 'rigorous correlation' need not be shown in order to establish practical utility; 'reasonable correlation' suffices." *Id.* (emphasis added). The Court also rejected Fujikawa's reliance on two articles. The Court noted that while one article taught that "*in vitro* testing is sometimes not a good indicator of how potent a compound will be *in vivo*, it does imply that compounds which are active *in vitro* will normally exhibit some *in vivo* activity." *Id.* at 1566. Similarly, the Court noted that the second article expressly stated that "[f]or most substances, although not for all, the relative potency determined in *in vitro* ... parallels the *in vivo* activity." *Id.*

The Court concluded that the facts in the case were analogous to the ones in *Cross* where the court relied on a known reasonable correlation between *in vitro* tests and *in vivo* activity, and therefore affirmed the Board's decision that Wattanasin had established a practical utility with the *in vitro* results. *Id.* at 1565-66.

The *Nelson*, *Cross*, and *Fujikawa* cases are very similar to the present case. The reasoning of the courts in all three cases that "[i]t is inherently faster and easier to combat illnesses and alleviate symptoms when the medical profession is armed with an arsenal of chemicals having known pharmacological activities" applies to the asserted utility for the claimed antibodies. *Fujikawa*, 93 F.3d at 1564, quoting *Nelson*, 626 F.2d at 856; see also *Cross*, 753 F.2d at 1051 ("Successful *in vitro* testing will marshal resources and direct the expenditure of effort to further *in vivo* testing of the most potent compounds, thereby providing an immediate benefit to the public, analogous to the benefit provided by the showing of an *in vivo* utility."). Like pharmaceutical compounds, nucleic acids, polypeptides, and antibodies which are associated with cancer will make it inherently faster and easier to combat cancer. The greater the

number of biological markers of cancer medical professionals have access to, the more accurate and detailed a diagnosis they can make. The determination that a gene is differentially expressed in cancer constitutes at least as significant a development in the field of cancer diagnostics as *in vitro* screening for pharmaceutical activity. See *Cross*, 753 F.2d at 1051 (“the first link in the screening chain, *in vitro* testing, may establish a practical utility for the compound in question. Successful *in vitro* testing will marshal resources and direct the expenditure of effort to further *in vivo* testing of the most potent compounds, thereby providing an immediate benefit to the public.”).

In addition, like *in vitro* tests in the pharmaceutical industry, those of skill in the field of biotechnology rely on the reasonable correlation that exists between gene expression and protein expression (see discussion *supra*). Were there no reasonable correlation between the two, the techniques that measure gene levels such as microarray analysis, differential display, and quantitative PCR would not be so widely used by those in the art. See *Second Grimaldi Declaration* at ¶ 5. As in *Cross*, Appellants here do not argue that there is “an invariable exact correlation” between gene expression and protein expression. See *Cross*, 753 F.2d at 1050. Instead, Appellants’ position detailed above is that a measured change in gene expression in cancer cells establishes a “significant probability” that the expression of the encoded polypeptide in cancer will also be changed based on “a reasonable correlation therebetween.” *Id.*; see also *Fujikawa*, 93 F.3d at 1565 (“a ‘rigorous correlation’ need not be shown in order to establish practical utility; ‘reasonable correlation’ suffices”); *Nelson*, 626 F.2d at 857 (holding that “a rigorous correlation is not necessary” and that a “reasonable correlation” will suffice).

Also of importance is the Court’s rejection of the notion that any *in vitro* testing must be statistically significant to support a practical utility. *Nelson*, 626 F.2d at 857. Likewise, qualitative characterizations of a test compound as either increasing or decreasing blood pressure was acceptable. *Id.* at 855 (stating that responses were categorized as either a depressor (lowering) effect or a pressor (elevating) effect). This is similar to the data in Example 18, where the change in mRNA levels is described as “more highly expressed.”

There are additional similarities. In *Fujikawa*, the Board and Court rejected the argument that there was no utility because there was no exact correlation between the *in vitro* and *in vivo* results in spite of supporting testimony and references. *Fujikawa*, 93 F.3d at 1565-66. Like the two references rejected by the Board and Court in *Fujikawa*, the *Chen et al.* reference cited by

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the Examiner may suggest that the correlation between changes in mRNA levels and protein levels is not exact. But like *Fujikawa*, portions of *Chen et al.* also support Appellants' assertion, and Appellants have submitted the declaration of two experts in the field which state that those in the field rely on the correlation between changes in mRNA and protein. See *Second Grimaldi Declaration* at ¶ 5; *Polakis Declaration* at ¶ 6. Thus, as was the case in *Fujikawa*, although there may be some evidence that the correlation relied on is not exact, the declarations and numerous references submitted by Appellants is more than enough evidence to establish that there is a "reasonable correlation" between changes in mRNA levels and changes in the level of the encoded protein.

In conclusion, Appellants have asserted that the claimed antibodies are useful for the diagnosis of cancer, particularly esophageal and skin cancer based on the data in Example 18. This utility is far beyond the nebulous expressions "biological activity" or "biological properties" rejected in *In re Kirk*, 376 F.2d 936, 153 U.S.P.Q. 48 (C.C.P.A. 1967). Like *Nelson*, *Cross*, and *Fujikawa*, Appellants have asserted a utility which relies on a reasonable correlation between the data disclosed in the application and the asserted utility. The fact that there may be limited evidence that the correlation is not exact does not invalidate Appellants' showing of utility since the correlation need not be a rigorous or exact one. Considering the relevant evidence as a whole, Appellants have provided sufficient evidence to establish a reasonable correlation between changes in the level of mRNA and corresponding changes in the level of the encoded polypeptide. Therefore the claimed antibodies have a practical utility as diagnostic tools for esophageal and skin cancer.

11. Utility – Conclusion

Appellants' asserted utility for the claimed antibodies as diagnostic tools for cancer corresponds in scope to the subject matter sought to be patented and therefore "must be taken as sufficient to satisfy the utility requirement of § 101 for the entire claimed subject." *In re Langer*, 503 F.2d 1380, 1391, 183 U.S.P.Q. 288, 297 (C.C.P.A. 1974). The Examiner's unsupported arguments and references are not sufficient evidence to make a *prima facie* showing that "one of ordinary skill in the art would reasonably doubt the asserted utility." *In re Brana*, 51 F.3d 1560, 1566, 34 U.S.P.Q.2d 1436 (Fed. Cir. 1995).

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And even if the Examiner has established a *prima facie* case, Appellants have offered sufficient rebuttal evidence in the form of expert declarations and references, which, when considered as a whole, establish that it is more likely than not that the asserted utility is true. *See In re Oetiker*, 977 F.2d 1443, 1445, 24 U.S.P.Q.2d 1443, 1444 (Fed. Cir. 1992) (stating that the evidentiary standard to be used throughout *ex parte* examination in setting forth a rejection is a preponderance of the evidence, or “more likely than not” standard); *M.P.E.P.* at § 2107.02, part VII (“evidence will be sufficient if, considered as a whole, it leads a person of ordinary skill in the art to conclude that the asserted utility is more likely than not true.”) (emphasis in original).

Finally, the courts’ decisions in similar cases make clear that the evidence provided by Appellants is sufficient to establish the asserted utility. The evidence does not need to be direct evidence, nor does it need to provide an exact correlation between the submitted evidence and the asserted utility. Instead, evidence which is “reasonably” correlated with the asserted utility is sufficient. *See Fujikawa*, 93 F.3d at 1565 (“a ‘rigorous correlation’ need not be shown in order to establish practical utility; ‘reasonable correlation’ suffices”); *Cross*, 753 F.2d at 1050 (same); *Nelson*, 626 F.2d at 857 (same). Considering the evidence as a whole in light of the relevant cases, the Board should find that Appellants have established at least one specific, substantial, and credible utility, and the Examiner’s rejection of the pending claims as lacking utility should be reversed.

C. Enablement Rejection – Detailed Argument

The second issue before the Board is whether Appellants have enabled the pending claims such that one of skill in the art would be able to make and use the claimed invention. The Examiner has rejected Claims 1-5 under 35 U.S.C. §112, first paragraph, arguing that because the claimed invention is not supported by either a specific or substantial asserted utility or a well-established utility, one skilled in the art clearly would not know how to use the claimed invention. *See First Office Action* at 8; *Final Office Action* at 3.

1. *Because the Claimed Invention is Supported by a Specific, Substantial and Credible Utility, the Enablement Rejection should be Reversed*

For the reasons stated above, the claimed invention is supported by a specific, substantial and credible utility. Because the lack of a supporting utility is the only basis for the Examiner’s

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rejection under 35 U.S.C. § 112, first paragraph, the Board should reverse the rejection of Claims 1-5 as lacking enablement.

D. Conclusion

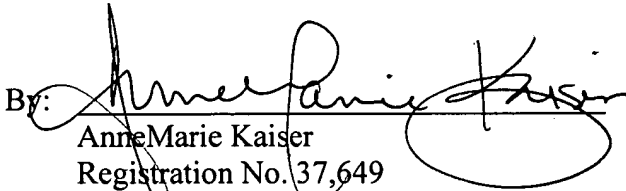
In view of the arguments presented above, Appellants submit that the specification as filed provides a specific, substantial and credible utility for the claimed antibodies and request withdrawal of the rejection under 35 U.S.C. §101, and the related rejection under 35 U.S.C. §112.

Please charge any additional fees, including any fees for additional extension of time, or credit overpayment to Deposit Account No. 11-1410.

Respectfully submitted,

KNOBBE, MARTENS, OLSON & BEAR, LLP

Dated: Sept. 29, 2005

By: 
Anne Marie Kaiser
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VIII. APPENDIX A – CLAIMS ON APPEAL

1. An isolated antibody that specifically binds to the polypeptide of SEQ ID NO:34.
2. The antibody of Claim 1 which is a monoclonal antibody.
3. The antibody of Claim 1 which is a humanized antibody.
4. The antibody of Claim 1 which is an antibody fragment.
5. The antibody of Claim 1 which is labeled.

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IX. APPENDIX B – EVIDENCE

Attached hereto is a copy of the evidence cited in Appellants' Brief. The list of evidence below is accompanied by a statement setting forth where in the record that evidence was entered into the record by the Examiner.

Tab	Reference	Submitted	Entered
1	Pennica <i>et al.</i> (Proc. Natl. Acad. Sci. USA (1998) 95:14717-14722)		Cited by Examiner in the first Office Action
2	Sen <i>et al.</i> (Curr. Opin. Oncol. (2000) 12: 82-88)		Cited by Examiner in the first Office Action
3	Hu <i>et al.</i> (J. Proteome Res., (2003) 2(4):405-12)		Cited by Examiner in the final Office Action
4	First Declaration of J. Christopher Grimaldi	Originally Submitted with Appellants' Amendment and Response to Office Action as Exhibit 2	Entered by Examiner in final Office Action
5	Haynes <i>et al.</i> (Electrophoresis, (1998) 19(11):1862-71)		Cited by Examiner in the final Office Action
6	Chen <i>et al.</i> (Mol. and Cell. Proteomics, (2002) 1:304-313)		Cited by Examiner in the final Office Action
7	Gygi <i>et al.</i> , Molecular and Cellular Biology, Mar. 1999, 1720-1730	Originally Submitted with Appellants' Amendment and Response to Final Office Action as Exhibit 5	Entered by Examiner in Advisory Action as confirmed by Examiner in telephone conversation
8	Second Declaration by J. Christopher Grimaldi	Originally submitted with Appellants' Amendment and Response to Office Action as Exhibit 6	Entered by Examiner in final Office Action
9	Declaration of Paul Polakis, Ph.D.	Originally submitted with Appellants' Amendment and Response to Office Action as Exhibit 7	Entered by Examiner in final Office Action
10	Bruce Alberts, <i>et al.</i> , Molecular Biology of the Cell (3 rd ed. 1994) hereinafter "Cell 3 rd ")	Originally submitted with Appellants' Amendment and Response to Final Office Action as Exhibit 6	Entered by Examiner in Advisory Action as confirmed by Examiner in telephone conversation

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11	Bruce Alberts, <i>et al.</i> , Molecular Biology of the Cell (4 th ed. 2002)	Originally submitted with Appellants' Amendment and Response to Final Office Action as Exhibit 7	Entered by Examiner in Advisory Action as confirmed by Examiner in telephone conversation
12	Benjamin Lewin, Genes VI (1997)	Originally submitted with Appellants' Amendment and Response to Final Office Action as Exhibit 8	Entered by Examiner in Advisory Action as confirmed by Examiner in telephone conversation
13	Zhigang <i>et al.</i> , World Journal of Surgical Oncology 2:13, 2004	Originally submitted with Appellants' Amendment and Response to Final Office Action as Exhibit 9	Entered by Examiner in Advisory Action as confirmed by Examiner in telephone conversation
14	Meric <i>et al.</i> , Molecular Cancer Therapeutics, vol. 1, 971-979 (2002)	Originally submitted with Appellants' Amendment and Response to Final Office Action as Exhibit 10	Entered by Examiner in Advisory Action as confirmed by Examiner in telephone conversation
15	Page 122 of the 2002- 2003 New England Biolabs catalog.	Originally submitted with Appellants' Amendment and Response to Final Office Action as Exhibit 1	Entered by Examiner in Advisory Action as confirmed by Examiner in telephone conversation

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X. APPENDIX C – RELATED PROCEEDINGS

There are no decisions rendered by a court or the Board in any related proceedings identified above.

WISP genes are members of the connective tissue growth factor family that are up-regulated in Wnt-1-transformed cells and aberrantly expressed in human colon tumors

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Contributed by David Botstein and Arnold J. Levine, October 21, 1998

ABSTRACT Wnt family members are critical to many developmental processes, and components of the Wnt signaling pathway have been linked to tumorigenesis in familial and sporadic colon carcinomas. Here we report the identification of two genes, *WISP-1* and *WISP-2*, that are up-regulated in the mouse mammary epithelial cell line C57MG transformed by Wnt-1, but not by Wnt-4. Together with a third related gene, *WISP-3*, these proteins define a subfamily of the connective tissue growth factor family. Two distinct systems demonstrated *WISP* induction to be associated with the expression of Wnt-1. These included (i) C57MG cells infected with a Wnt-1 retroviral vector or expressing Wnt-1 under the control of a tetracycline repressible promoter, and (ii) Wnt-1 transgenic mice. The *WISP-1* gene was localized to human chromosome 8q24.1–8q24.3. *WISP-1* genomic DNA was amplified in colon cancer cell lines and in human colon tumors and its RNA overexpressed (2- to >30-fold) in 84% of the tumors examined compared with patient-matched normal mucosa. *WISP-3* mapped to chromosome 6q22–6q23 and also was overexpressed (4- to >40-fold) in 63% of the colon tumors analyzed. In contrast, *WISP-2* mapped to human chromosome 20q12–20q13 and its DNA was amplified, but RNA expression was reduced (2- to >30-fold) in 79% of the tumors. These results suggest that the *WISP* genes may be downstream of Wnt-1 signaling and that aberrant levels of *WISP* expression in colon cancer may play a role in colon tumorigenesis.

Wnt-1 is a member of an expanding family of cysteine-rich, glycosylated signaling proteins that mediate diverse developmental processes such as the control of cell proliferation, adhesion, cell polarity, and the establishment of cell fates (1, 2). Wnt-1 originally was identified as an oncogene activated by the insertion of mouse mammary tumor virus in virus-induced mammary adenocarcinomas (3, 4). Although Wnt-1 is not expressed in the normal mammary gland, expression of Wnt-1 in transgenic mice causes mammary tumors (5).

In mammalian cells, Wnt family members initiate signaling by binding to the seven-transmembrane spanning Frizzled receptors and recruiting the cytoplasmic protein Dishevelled (Dsh) to the cell membrane (1, 2, 6). Dsh then inhibits the kinase activity of the normally constitutively active glycogen synthase kinase-3 β (GSK-3 β) resulting in an increase in β -catenin levels. Stabilized β -catenin interacts with the transcription factor TCF/Lef1, forming a complex that appears in

the nucleus and binds TCF/Lef1 target DNA elements to activate transcription (7, 8). Other experiments suggest that the adenomatous polyposis coli (APC) tumor suppressor gene also plays an important role in Wnt signaling by regulating β -catenin levels (9). APC is phosphorylated by GSK-3 β , binds to β -catenin, and facilitates its degradation. Mutations in either APC or β -catenin have been associated with colon carcinomas and melanomas, suggesting these mutations contribute to the development of these types of cancer, implicating the Wnt pathway in tumorigenesis (1).

Although much has been learned about the Wnt signaling pathway over the past several years, only a few of the transcriptionally activated downstream components activated by Wnt have been characterized. Those that have been described cannot account for all of the diverse functions attributed to Wnt signaling. Among the candidate Wnt target genes are those encoding the nodal-related 3 gene, *Xnr3*, a member of the transforming growth factor (TGF)- β superfamily, and the homeobox genes, *engrailed*, *gooseoid*, *twin* (*Xtwn*), and *siamois* (2). A recent report also identifies *c-myc* as a target gene of the Wnt signaling pathway (10).

To identify additional downstream genes in the Wnt signaling pathway that are relevant to the transformed cell phenotype, we used a PCR-based cDNA subtraction strategy, suppression subtractive hybridization (SSH) (11), using RNA isolated from C57MG mouse mammary epithelial cells and C57MG cells stably transformed by a Wnt-1 retrovirus. Overexpression of Wnt-1 in this cell line is sufficient to induce a partially transformed phenotype, characterized by elongated and refractile cells that lose contact inhibition and form a multilayered array (12, 13). We reasoned that genes differentially expressed between these two cell lines might contribute to the transformed phenotype.

In this paper, we describe the cloning and characterization of two genes up-regulated in Wnt-1 transformed cells, *WISP-1* and *WISP-2*, and a third related gene, *WISP-3*. The *WISP* genes are members of the CCN family of growth factors, which includes connective tissue growth factor (CTGF), Cyr61, and *nov*, a family not previously linked to Wnt signaling.

MATERIALS AND METHODS

SSH. SSH was performed by using the PCR-Select cDNA Subtraction Kit (CLONTECH). Tester double-stranded

Abbreviations: TGF, transforming growth factor; CTGF, connective tissue growth factor; SSH, suppression subtractive hybridization; VWC, von Willebrand factor type C module.

Data deposition: The sequences reported in this paper have been deposited in the Genbank database (accession nos. AF100777, AF100778, AF100779, AF100780, and AF100781).

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cDNA was synthesized from 2 μ g of poly(A)⁺ RNA isolated from the C57MG/Wnt-1 cell line and driver cDNA from 2 μ g of poly(A)⁺ RNA from the parent C57MG cells. The subtracted cDNA library was subcloned into a pGEM-T vector for further analysis.

cDNA Library Screening. Clones encoding full-length mouse *WISP-1* were isolated by screening a λ gt10 mouse embryo cDNA library (CLONTECH) with a 70-bp probe from the original partial clone 568 sequence corresponding to amino acids 128–169. Clones encoding full-length human *WISP-1* were isolated by screening λ gt10 lung and fetal kidney cDNA libraries with the same probe at low stringency. Clones encoding full-length mouse and human *WISP-2* were isolated by screening a C57MG/Wnt-1 or human fetal lung cDNA library with a probe corresponding to nucleotides 1463–1512. Full-length cDNAs encoding *WISP-3* were cloned from human bone marrow and fetal kidney libraries.

Expression of Human *WISP* RNA. PCR amplification of first-strand cDNA was performed with human Multiple Tissue cDNA panels (CLONTECH) and 300 μ M of each dNTP at 94°C for 1 sec, 62°C for 30 sec, 72°C for 1 min, for 22–32 cycles. *WISP* and glyceraldehyde-3-phosphate dehydrogenase primer sequences are available on request.

In Situ Hybridization. ³³P-labeled sense and antisense riboprobes were transcribed from an 897-bp PCR product corresponding to nucleotides 601–1440 of mouse *WISP-1* or a 294-bp PCR product corresponding to nucleotides 82–375 of mouse *WISP-2*. All tissues were processed as described (40).

Radiation Hybrid Mapping. Genomic DNA from each hybrid in the Stanford G3 and Genebridge4 Radiation Hybrid Panels (Research Genetics, Huntsville, AL) and human and hamster control DNAs were PCR-amplified, and the results were submitted to the Stanford or Massachusetts Institute of Technology web servers.

Cell Lines, Tumors, and Mucosa Specimens. Tissue specimens were obtained from the Department of Pathology (University of Pittsburgh) for patients undergoing colon resection and from the University of Leeds, United Kingdom. Genomic DNA was isolated (Qiagen) from the pooled blood of 10 normal human donors, surgical specimens, and the following ATCC human cell lines: SW480, COLO 320DM, HT-29, WiDr, and SW403 (colon adenocarcinomas), SW620 (lymph node metastasis, colon adenocarcinoma), HCT 116 (colon carcinoma), SK-CO-1 (colon adenocarcinoma, ascites), and HM7 (a variant of ATCC colon adenocarcinoma cell line LS 174T). DNA concentration was determined by using Hoechst dye 33258 intercalation fluorimetry. Total RNA was prepared by homogenization in 7 M GuSCN followed by centrifugation over CsCl cushions or prepared by using RNeasy.

Gene Amplification and RNA Expression Analysis. Relative gene amplification and RNA expression of *WISPs* and *c-myc* in the cell lines, colorectal tumors, and normal mucosa were determined by quantitative PCR. Gene-specific primers and fluorogenic probes (sequences available on request) were designed and used to amplify and quantitate the genes. The relative gene copy number was derived by using the formula $2^{\Delta\Delta C_t}$ where ΔC_t represents the difference in amplification cycles required to detect the *WISP* genes in peripheral blood lymphocyte DNA compared with colon tumor DNA or colon tumor RNA compared with normal mucosal RNA. The Δ -method was used for calculation of the SE of the gene copy number or RNA expression level. The *WISP*-specific signal was normalized to that of the glyceraldehyde-3-phosphate dehydrogenase housekeeping gene. All TaqMan assay reagents were obtained from Perkin-Elmer Applied Biosystems.

RESULTS

Isolation of *WISP-1* and *WISP-2* by SSH. To identify Wnt-1-inducible genes, we used the technique of SSH using the

mouse mammary epithelial cell line C57MG and C57MG cells that stably express Wnt-1 (11). Candidate differentially expressed cDNAs (1,384 total) were sequenced. Thirty-nine percent of the sequences matched known genes or homologues, 32% matched expressed sequence tags, and 29% had no match. To confirm that the transcript was differentially expressed, semiquantitative reverse transcription-PCR and Northern analysis were performed by using mRNA from the C57MG and C57MG/Wnt-1 cells.

Two of the cDNAs, *WISP-1* and *WISP-2*, were differentially expressed, being induced in the C57MG/Wnt-1 cell line, but not in the parent C57MG cells or C57MG cells overexpressing Wnt-4 (Fig. 1A and B). Wnt-4, unlike Wnt-1, does not induce the morphological transformation of C57MG cells and has no effect on β -catenin levels (13, 14). Expression of *WISP-1* was up-regulated approximately 3-fold in the C57MG/Wnt-1 cell line and *WISP-2* by approximately 5-fold by both Northern analysis and reverse transcription-PCR.

An independent, but similar, system was used to examine *WISP* expression after Wnt-1 induction. C57MG cells expressing the *Wnt-1* gene under the control of a tetracycline-repressible promoter produce low amounts of Wnt-1 in the repressed state but show a strong induction of *Wnt-1* mRNA and protein within 24 hr after tetracycline removal (8). The levels of Wnt-1 and *WISP* RNA isolated from these cells at various times after tetracycline removal were assessed by quantitative PCR. Strong induction of Wnt-1 mRNA was seen as early as 10 hr after tetracycline removal. Induction of *WISP* mRNA (2- to 6-fold) was seen at 48 and 72 hr (data not shown). These data support our previous observations that show that *WISP* induction is correlated with Wnt-1 expression. Because the induction is slow, occurring after approximately 48 hr, the induction of *WISPs* may be an indirect response to Wnt-1 signaling.

cDNA clones of human *WISP-1* were isolated and the sequence compared with mouse *WISP-1*. The cDNA sequences of mouse and human *WISP-1* were 1,766 and 2,830 bp in length, respectively, and encode proteins of 367 aa, with predicted relative molecular masses of \approx 40,000 (M_r 40 K). Both have hydrophobic N-terminal signal sequences, 38 conserved cysteine residues, and four potential N-linked glycosylation sites and are 84% identical (Fig. 2A).

Full-length cDNA clones of mouse and human *WISP-2* were 1,734 and 1,293 bp in length, respectively, and encode proteins of 251 and 250 aa, respectively, with predicted relative molecular masses of \approx 27,000 (M_r 27 K) (Fig. 2B). Mouse and human *WISP-2* are 73% identical. Human *WISP-2* has no potential N-linked glycosylation sites, and mouse *WISP-2* has one at

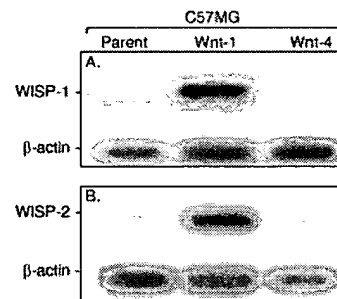


Fig. 1. *WISP-1* and *WISP-2* are induced by Wnt-1, but not Wnt-4, expression in C57MG cells. Northern analysis of *WISP-1* (A) and *WISP-2* (B) expression in C57MG, C57MG/Wnt-1, and C57MG/Wnt-4 cells. Poly(A)⁺ RNA (2 μ g) was subjected to Northern blot analysis and hybridized with a 70-bp mouse *WISP-1*-specific probe (amino acids 278–300) or a 190-bp *WISP-2*-specific probe (nucleotides 1438–1627) in the 3' untranslated region. Blots were rehybridized with human β -actin probe.

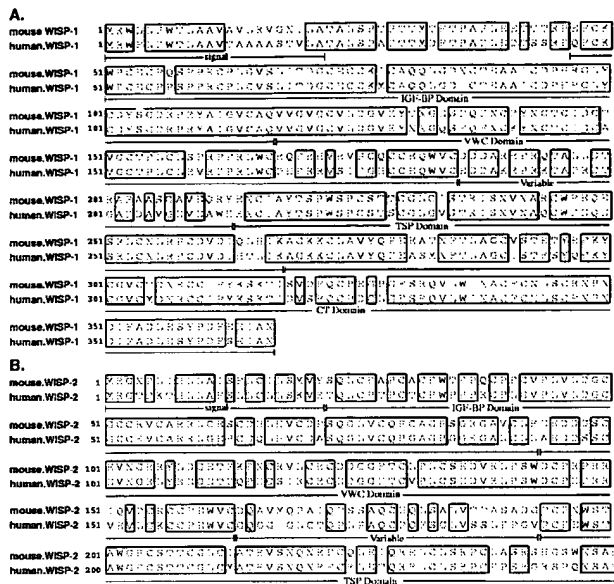


FIG. 2. Encoded amino acid sequence alignment of mouse and human *WISP-1* (A) and mouse and human *WISP-2* (B). The potential signal sequence, insulin-like growth factor-binding protein (IGF-BP), VWC, thrombospondin (TSP), and C-terminal (CT) domains are underlined.

position 197. *WISP-2* has 28 cysteine residues that are conserved among the 38 cysteines found in *WISP-1*.

Identification of *WISP-3*. To search for related proteins, we screened expressed sequence tag (EST) databases with the *WISP-1* protein sequence and identified several ESTs as potentially related sequences. We identified a homologous protein that we have called *WISP-3*. A full-length human *WISP-3* cDNA of 1,371 bp was isolated corresponding to those ESTs that encode a 354-aa protein with a predicted molecular mass of 39,293. *WISP-3* has two potential N-linked glycosylation sites and 36 cysteine residues. An alignment of the three human *WISP* proteins shows that *WISP-1* and *WISP-3* are the most similar (42% identity), whereas *WISP-2* has 37% identity with *WISP-1* and 32% identity with *WISP-3* (Fig. 3A).

***WISPs* Are Homologous to the CTGF Family of Proteins.** Human *WISP-1*, *WISP-2*, and *WISP-3* are novel sequences; however, mouse *WISP-1* is the same as the recently identified *Elm1* gene. *Elm1* is expressed in low, but not high, metastatic mouse melanoma cells, and suppresses the *in vivo* growth and metastatic potential of K-1735 mouse melanoma cells (15). Human and mouse *WISP-2* are homologous to the recently described rat gene, *rCop-1* (16). Significant homology (36–44%) was seen to the CCN family of growth factors. This family includes three members, CTGF, Cyr61, and the protooncogene *nov*. CTGF is a chemotactic and mitogenic factor for fibroblasts that is implicated in wound healing and fibrotic disorders and is induced by TGF- β (17). Cyr61 is an extracellular matrix signaling molecule that promotes cell adhesion, proliferation, migration, angiogenesis, and tumor growth (18, 19). *nov* (nephroblastoma overexpressed) is an immediate early gene associated with quiescence and found altered in Wilms tumors (20). The proteins of the CCN family share functional, but not sequence, similarity to Wnt-1. All are secreted, cysteine-rich heparin binding glycoproteins that associate with the cell surface and extracellular matrix.

WISP proteins exhibit the modular architecture of the CCN family, characterized by four conserved cysteine-rich domains (Fig. 3B) (21). The N-terminal domain, which includes the first 12 cysteine residues, contains a consensus sequence (GCGC-CXXC) conserved in most insulin-like growth factor (IGF)-

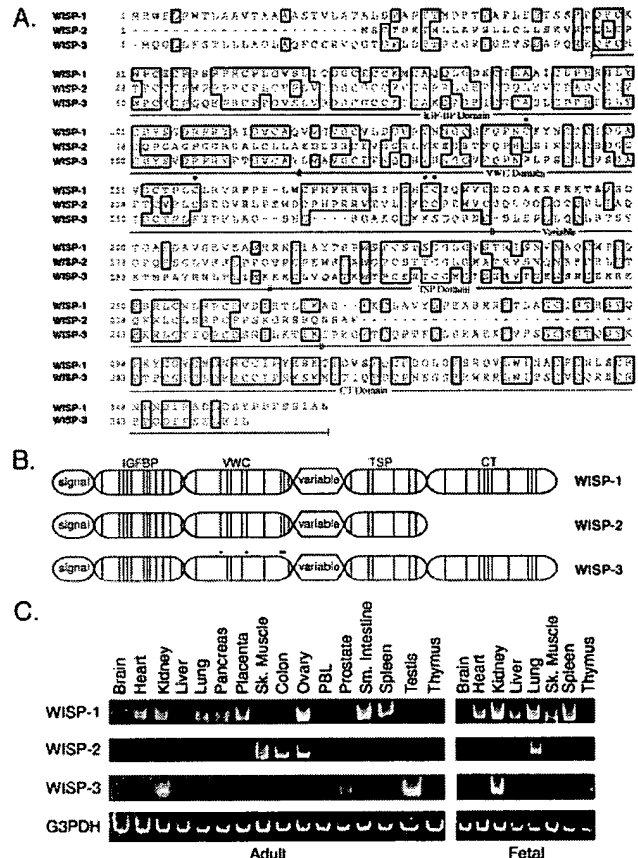


FIG. 3. (A) Encoded amino acid sequence alignment of human *WISPs*. The cysteine residues of *WISP-1* and *WISP-2* that are not present in *WISP-3* are indicated with a dot. (B) Schematic representation of the *WISP* proteins showing the domain structure and cysteine residues (vertical lines). The four cysteine residues in the VWC domain that are absent in *WISP-3* are indicated with a dot. (C) Expression of *WISP* mRNA in human tissues. PCR was performed on human multiple-tissue cDNA panels (CLONTECH) from the indicated adult and fetal tissues.

binding proteins (BP). This sequence is conserved in *WISP-2* and *WISP-3*, whereas *WISP-1* has a glutamine in the third position instead of a glycine. CTGF recently has been shown to specifically bind IGF (22) and a truncated *nov* protein lacking the IGF-BP domain is oncogenic (23). The von Willebrand factor type C module (VWC), also found in certain collagens and mucins, covers the next 10 cysteine residues, and is thought to participate in protein complex formation and oligomerization (24). The VWC domain of *WISP-3* differs from all CCN family members described previously, in that it contains only six of the 10 cysteine residues (Fig. 3A and B). A short variable region follows the VWC domain. The third module, the thrombospondin (TSP) domain is involved in binding to sulfated glycoconjugates and contains six cysteine residues and a conserved WSxCSSxCG motif first identified in thrombospondin (25). The C-terminal (CT) module containing the remaining 10 cysteines is thought to be involved in dimerization and receptor binding (26). The CT domain is present in all CCN family members described to date but is absent in *WISP-2* (Fig. 3A and B). The existence of a putative signal sequence and the absence of a transmembrane domain suggest that *WISPs* are secreted proteins, an observation supported by an analysis of their expression and secretion from mammalian cell and baculovirus cultures (data not shown).

Expression of *WISP* mRNA in Human Tissues. Tissue-specific expression of human *WISPs* was characterized by PCR

analysis on adult and fetal multiple tissue cDNA panels. *WISP-1* expression was seen in the adult heart, kidney, lung, pancreas, placenta, ovary, small intestine, and spleen (Fig. 3C). Little or no expression was detected in the brain, liver, skeletal muscle, colon, peripheral blood leukocytes, prostate, testis, or thymus. *WISP-2* had a more restricted tissue expression and was detected in adult skeletal muscle, colon, ovary, and fetal lung. Predominant expression of *WISP-3* was seen in adult kidney and testis and fetal kidney. Lower levels of *WISP-3* expression were detected in placenta, ovary, prostate, and small intestine.

In Situ Localization of *WISP-1* and *WISP-2*. Expression of *WISP-1* and *WISP-2* was assessed by *in situ* hybridization in mammary tumors from Wnt-1 transgenic mice. Strong expression of *WISP-1* was observed in stromal fibroblasts lying within the fibrovascular tumor stroma (Fig. 4 A–D). However, low-level *WISP-1* expression also was observed focally within tumor cells (data not shown). No expression was observed in normal breast. Like *WISP-1*, *WISP-2* expression also was seen in the tumor stroma in breast tumors from Wnt-1 transgenic animals (Fig. 4 E–H). However, *WISP-2* expression in the stroma was in spindle-shaped cells adjacent to capillary vessels, whereas

the predominant cell type expressing *WISP-1* was the stromal fibroblasts.

Chromosome Localization of the *WISP* Genes. The chromosomal location of the human *WISP* genes was determined by radiation hybrid mapping panels. *WISP-1* is approximately 3.48 cR from the meiotic marker AFM259xc5 [logarithm of odds (lod) score 16.31] on chromosome 8q24.1 to 8q24.3, in the same region as the human locus of the *novH* family member (27) and roughly 4 Mbs distal to *c-myc* (28). Preliminary fine mapping indicates that *WISP-1* is located near D8S1712 STS. *WISP-2* is linked to the marker SHGC-33922 (lod = 1,000) on chromosome 20q12–20q13.1. Human *WISP-3* mapped to chromosome 6q22–6q23 and is linked to the marker AFM211ze5 (lod = 1,000). *WISP-3* is approximately 18 Mbs proximal to CTGF and 23 Mbs proximal to the human cellular oncogene *MYB* (27, 29).

Amplification and Aberrant Expression of *WISPs* in Human Colon Tumors. Amplification of protooncogenes is seen in many human tumors and has etiological and prognostic significance. For example, in a variety of tumor types, *c-myc* amplification has been associated with malignant progression and poor prognosis (30). Because *WISP-1* resides in the same general chromosomal location (8q24) as *c-myc*, we asked whether it was a target of gene amplification, and, if so, whether this amplification was independent of the *c-myc* locus. Genomic DNA from human colon cancer cell lines was assessed by quantitative PCR and Southern blot analysis. (Fig. 5 A and B). Both methods detected similar degrees of *WISP-1* amplification. Most cell lines showed significant (2- to 4-fold) amplification, with the HT-29 and WiDr cell lines demonstrating an 8-fold increase. Significantly, the pattern of amplification observed did not correlate with that observed for *c-myc*, indicating that the *c-myc* gene is not part of the amplicon that involves the *WISP-1* locus.

We next examined whether the *WISP* genes were amplified in a panel of 25 primary human colon adenocarcinomas. The relative *WISP* gene copy number in each colon tumor DNA was compared with pooled normal DNA from 10 donors by quantitative PCR (Fig. 6). The copy number of *WISP-1* and *WISP-2* was significantly greater than one, approximately 2-fold for *WISP-1* in about 60% of the tumors and 2- to 4-fold for *WISP-2* in 92% of the tumors ($P < 0.001$ for each). The copy number for *WISP-3* was indistinguishable from one ($P = 0.166$). In addition, the copy number of *WISP-2* was significantly higher than that of *WISP-1* ($P < 0.001$).

The levels of *WISP* transcripts in RNA isolated from 19 adenocarcinomas and their matched normal mucosa were

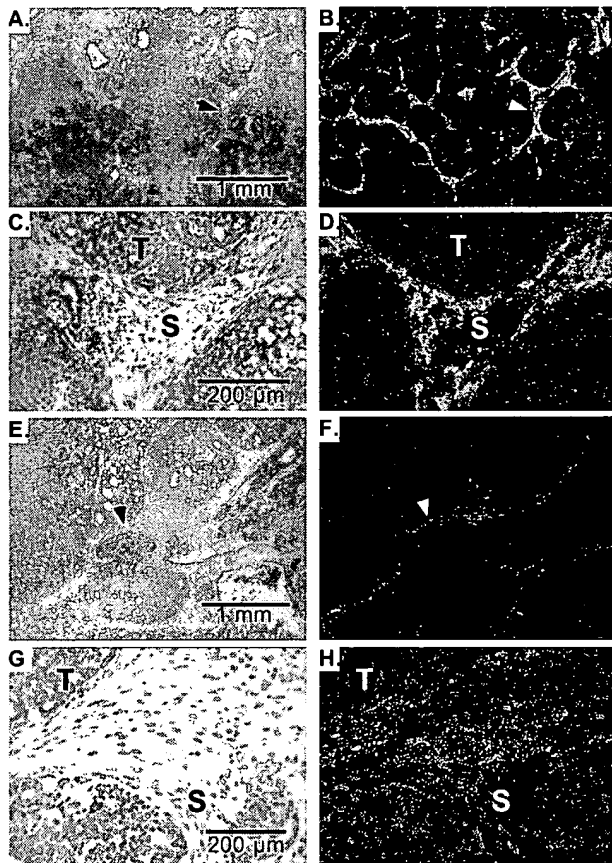


FIG. 4. (A, C, E, and G) Representative hematoxylin/eosin-stained images from breast tumors in Wnt-1 transgenic mice. The corresponding dark-field images showing *WISP-1* expression are shown in B and D. The tumor is a moderately well-differentiated adenocarcinoma showing evidence of adenoid cystic change. At low power (A and B), expression of *WISP-1* is seen in the delicate branching fibrovascular tumor stroma (arrowhead). At higher magnification, expression is seen in the stromal(s) fibroblasts (C and D), and tumor cells are negative. Focal expression of *WISP-1*, however, was observed in tumor cells in some areas. Images of *WISP-2* expression are shown in E–H. At low power (E and F), expression of *WISP-2* is seen in cells lying within the fibrovascular tumor stroma. At higher magnification, these cells appeared to be adjacent to capillary vessels whereas tumor cells are negative (G and H).

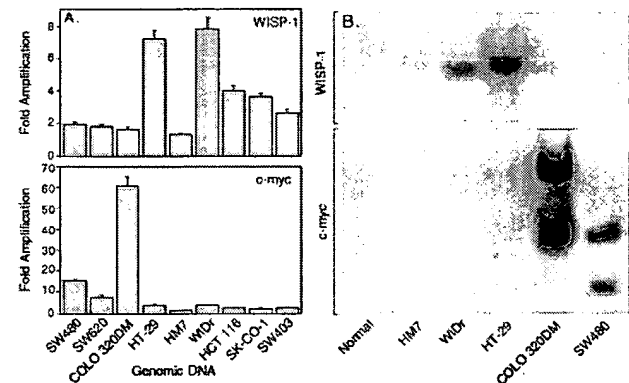


FIG. 5. Amplification of *WISP-1* genomic DNA in colon cancer cell lines. (A) Amplification in cell line DNA was determined by quantitative PCR. (B) Southern blots containing genomic DNA (10 μ g) digested with *EcoRI* (*WISP-1*) or *XbaI* (*c-myc*) were hybridized with a 100-bp human *WISP-1* probe (amino acids 186–219) or a human *c-myc* probe (located at bp 1901–2000). The *WISP* and *myc* genes are detected in normal human genomic DNA after a longer film exposure.

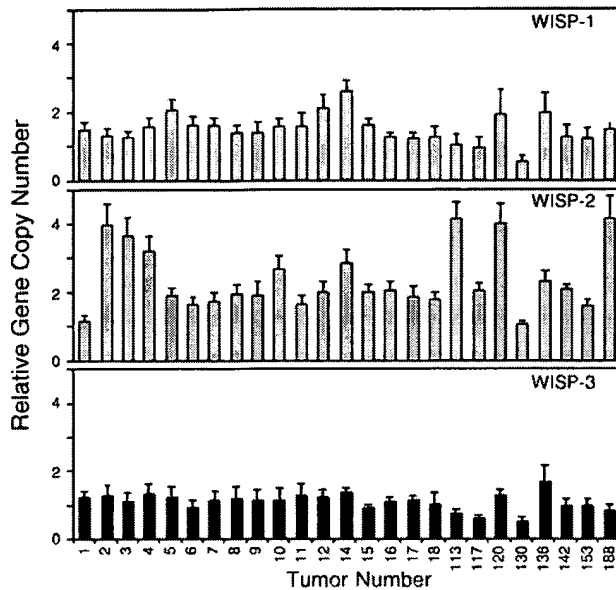


FIG. 6. Genomic amplification of *WISP* genes in human colon tumors. The relative gene copy number of the *WISP* genes in 25 adenocarcinomas was assayed by quantitative PCR, by comparing DNA from primary human tumors with pooled DNA from 10 healthy donors. The data are means \pm SEM from one experiment done in triplicate. The experiment was repeated at least three times.

assessed by quantitative PCR (Fig. 7). The level of *WISP-1* RNA present in tumor tissue varied but was significantly increased (2- to >25-fold) in 84% (16/19) of the human colon tumors examined compared with normal adjacent mucosa. Four of 19 tumors showed greater than 10-fold overexpression. In contrast, in 79% (15/19) of the tumors examined, *WISP-2* RNA expression was significantly lower in the tumor than the mucosa. Similar to *WISP-1*, *WISP-3* RNA was overexpressed in 63% (12/19) of the colon tumors compared with the normal

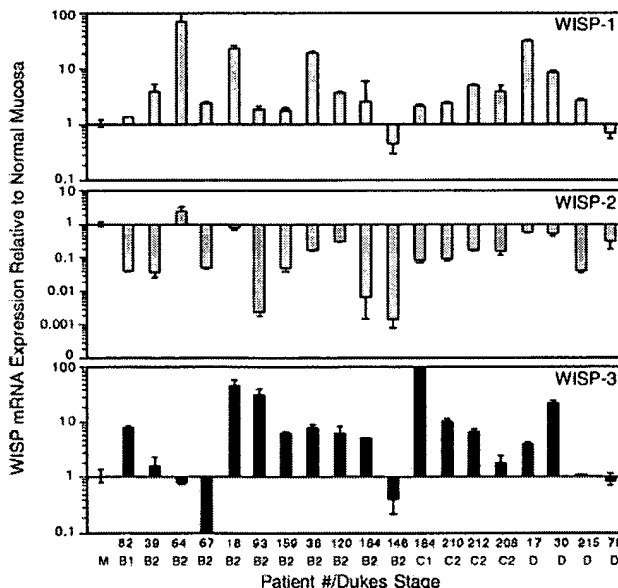


FIG. 7. *WISP* RNA expression in primary human colon tumors relative to expression in normal mucosa from the same patient. Expression of *WISP* mRNA in 19 adenocarcinomas was assayed by quantitative PCR. The Dukes stage of the tumor is listed under the sample number. The data are means \pm SEM from one experiment done in triplicate. The experiment was repeated at least twice.

mucosa. The amount of overexpression of *WISP-3* ranged from 4- to >40-fold.

DISCUSSION

One approach to understanding the molecular basis of cancer is to identify differences in gene expression between cancer cells and normal cells. Strategies based on assumptions that steady-state mRNA levels will differ between normal and malignant cells have been used to clone differentially expressed genes (31). We have used a PCR-based selection strategy, SSH, to identify genes selectively expressed in C57MG mouse mammary epithelial cells transformed by Wnt-1.

Three of the genes isolated, *WISP-1*, *WISP-2*, and *WISP-3*, are members of the CCN family of growth factors, which includes CTGF, Cyr61, and *nov*, a family not previously linked to Wnt signaling.

Two independent experimental systems demonstrated that *WISP* induction was associated with the expression of Wnt-1. The first was C57MG cells infected with a Wnt-1 retroviral vector or C57MG cells expressing Wnt-1 under the control of a tetracycline-repressible promoter, and the second was in Wnt-1 transgenic mice, where breast tissue expresses Wnt-1, whereas normal breast tissue does not. No *WISP* RNA expression was detected in mammary tumors induced by polyoma virus middle T antigen (data not shown). These data suggest a link between Wnt-1 and *WISPs* in that in these two situations, *WISP* induction was correlated with Wnt-1 expression.

It is not clear whether the *WISPs* are directly or indirectly induced by the downstream components of the Wnt-1 signaling pathway (i.e., β -catenin-TCF-1/Lef1). The increased levels of *WISP* RNA were measured in Wnt-1-transformed cells, hours or days after Wnt-1 transformation. Thus, *WISP* expression could result from Wnt-1 signaling directly through β -catenin transcription factor regulation or alternatively through Wnt-1 signaling turning on a transcription factor, which in turn regulates *WISPs*.

The *WISPs* define an additional subfamily of the CCN family of growth factors. One striking difference observed in the protein sequence of *WISP-2* is the absence of a CT domain, which is present in CTGF, Cyr61, *nov*, *WISP-1*, and *WISP-3*. This domain is thought to be involved in receptor binding and dimerization. Growth factors, such as TGF- β , platelet-derived growth factor, and nerve growth factor, which contain a cysteine knot motif exist as dimers (32). It is tempting to speculate that *WISP-1* and *WISP-3* may exist as dimers, whereas *WISP-2* exists as a monomer. If the CT domain is also important for receptor binding, *WISP-2* may bind its receptor through a different region of the molecule than the other CCN family members. No specific receptors have been identified for CTGF or *nov*. A recent report has shown that integrin $\alpha_v\beta_3$ serves as an adhesion receptor for Cyr61 (33).

The strong expression of *WISP-1* and *WISP-2* in cells lying within the fibrovascular tumor stroma in breast tumors from Wnt-1 transgenic animals is consistent with previous observations that transcripts for the related CTGF gene are primarily expressed in the fibrous stroma of mammary tumors (34). Epithelial cells are thought to control the proliferation of connective tissue stroma in mammary tumors by a cascade of growth factor signals similar to that controlling connective tissue formation during wound repair. It has been proposed that mammary tumor cells or inflammatory cells at the tumor interstitial interface secrete TGF- β 1, which is the stimulus for stromal proliferation (34). TGF- β 1 is secreted by a large percentage of malignant breast tumors and may be one of the growth factors that stimulates the production of CTGF and *WISPs* in the stroma.

It was of interest that *WISP-1* and *WISP-2* expression was observed in the stromal cells that surrounded the tumor cells

(epithelial cells) in the Wnt-1 transgenic mouse sections of breast tissue. This finding suggests that paracrine signaling could occur in which the stromal cells could supply WISP-1 and WISP-2 to regulate tumor cell growth on the WISP extracellular matrix. Stromal cell-derived factors in the extracellular matrix have been postulated to play a role in tumor cell migration and proliferation (35). The localization of *WISP-1* and *WISP-2* in the stromal cells of breast tumors supports this paracrine model.

An analysis of *WISP-1* gene amplification and expression in human colon tumors showed a correlation between DNA amplification and overexpression, whereas overexpression of *WISP-3* RNA was seen in the absence of DNA amplification. In contrast, *WISP-2* DNA was amplified in the colon tumors, but its mRNA expression was significantly reduced in the majority of tumors compared with the expression in normal colonic mucosa from the same patient. The gene for human *WISP-2* was localized to chromosome 20q12–20q13, at a region frequently amplified and associated with poor prognosis in node negative breast cancer and many colon cancers, suggesting the existence of one or more oncogenes at this locus (36–38). Because the center of the 20q13 amplicon has not yet been identified, it is possible that the apparent amplification observed for *WISP-2* may be caused by another gene in this amplicon.

A recent manuscript on *rCop-1*, the rat orthologue of *WISP-2*, describes the loss of expression of this gene after cell transformation, suggesting it may be a negative regulator of growth in cell lines (16). Although the mechanism by which *WISP-2* RNA expression is down-regulated during malignant transformation is unknown, the reduced expression of *WISP-2* in colon tumors and cell lines suggests that it may function as a tumor suppressor. These results show that the *WISP* genes are aberrantly expressed in colon cancer and suggest that their altered expression may confer selective growth advantage to the tumor.

Members of the Wnt signaling pathway have been implicated in the pathogenesis of colon cancer, breast cancer, and melanoma, including the tumor suppressor gene adenomatous polyposis coli and β -catenin (39). Mutations in specific regions of either gene can cause the stabilization and accumulation of cytoplasmic β -catenin, which presumably contributes to human carcinogenesis through the activation of target genes such as the *WISPs*. Although the mechanism by which Wnt-1 transforms cells and induces tumorigenesis is unknown, the identification of *WISPs* as genes that may be regulated downstream of Wnt-1 in C57MG cells suggests they could be important mediators of Wnt-1 transformation. The amplification and altered expression patterns of the *WISPs* in human colon tumors may indicate an important role for these genes in tumor development.

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Aneuploidy and cancer

Subrata Sen, PhD

Numeric aberrations in chromosomes, referred to as aneuploidy, is commonly observed in human cancer. Whether aneuploidy is a cause or consequence of cancer has long been debated. Three lines of evidence now make a compelling case for aneuploidy being a discrete chromosome mutation event that contributes to malignant transformation and progression process. First, precise assay of chromosome aneuploidy in several primary tumors with *in situ* hybridization and comparative genomic hybridization techniques have revealed that specific chromosome aneusomies correlate with distinct tumor phenotypes. Second, aneuploid tumor cell lines and *in vitro* transformed rodent cells have been reported to display an elevated rate of chromosome instability, thereby indicating that aneuploidy is a dynamic chromosome mutation event associated with transformation of cells. Third, and most important, a number of mitotic genes regulating chromosome segregation have been found mutated in human cancer cells, implicating such mutations in induction of aneuploidy in tumors. Some of these gene mutations, possibly allowing unequal segregations of chromosomes, also cause tumorigenic transformation of cells *in vitro*. In this review, the recent publications investigating aneuploidy in human cancers, rate of chromosome instability in aneuploidy tumor cells, and genes implicated in regulating chromosome segregation found mutated in cancer cells are discussed. *Curr Opin Oncol* 2000, 12:82-88 © 2000 Lippincott Williams & Wilkins, Inc.

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Abbreviations

CGH comparative genomic hybridization
CHE Chinese hamster embryo cells
FISH fluorescence *in situ* hybridization
HPRC hereditary papillary renal carcinoma
ISH *in situ* hybridization

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Cancer research over the past decade has firmly established that malignant cells accumulate a large number of genetic mutations that affect differentiation, proliferation, and cell death processes. In addition, it is also recognized that most cancers are clonal, although they display extensive heterogeneity with respect to karyotypes and phenotypes of individual clonal populations. It is estimated that numeric chromosomal imbalance, referred to as *aneuploidy*, is the most prevalent genetic change recorded among over 20,000 solid tumors analyzed thus far [1]. Phenotypic diversity of the clonal populations in individual tumors involve differences in morphology, proliferative properties, antigen expression, drug sensitivity, and metastatic potentials. It has been proposed that an underlying acquired genetic instability is responsible for the multiple mutations detected in cancer cells that lead to tumor heterogeneity and progression [2]. In a somewhat contradictory argument, it has also been suggested that clonal expansion due to selection of cells undergoing normal rates of mutation can explain malignant transformation and progression process in humans [3]. Acquired genetic instability, nonetheless, is considered important for more rapid progression of the disease [4••]. Although the original hypothesis on genetic instability in cancer primarily focused on chromosome imbalances in the form of aneuploidy in tumor cells, the actual relevance of such mutations in cancer remains a controversial issue.

Whether or not aneuploidy contributes to the malignant transformation and progression process has long been debated. A prevalent idea on genetics of cancer referred to as "somatic gene mutation hypothesis" contends that gene mutations at the nucleotide level alone can cause cancer by either activating cellular proto-oncogenes to dominant cancer causing oncogenes and/or by inactivating growth inhibitory tumor suppressor genes. In this scheme of things chromosomal instability in the form of aneuploidy is a mere consequence rather than a cause of malignant transformation and progression process.

In this review, some of the recent observations on the subject are discussed and compelling evidence is provided to suggest that aneuploidy is a distinct form of genetic instability in cancer that frequently correlates with specific phenotypes and stages of the disease. Furthermore, discrete genetic targets affecting chromosomal stability in cancer cells, recently identified, are also discussed. These data provide a new direction toward elucidating the molecular mechanisms responsi-

ble for induction of aneuploidy in cancer and may eventually be exploited as novel therapeutic targets in the future.

Genetic alterations in cancer

Alterations in many genetic loci regulating growth, senescence, and apoptosis, identified in tumor cells, have led to the current understanding of cancer as a genetic disease. The genetic changes identified in tumors include: subtle mutations in genes at the nucleotide level; chromosomal translocations leading to structural rearrangements in genes; and numeric changes in either partial segments of chromosomes or whole chromosomes (aneuploidy) causing imbalance in gene dosage.

For the purpose of this review, both segmental and whole chromosome imbalances leading to altered DNA dosage in cancer cells are included as examples of aneuploidy.

Incidence of aneuploidy in cancer

Evidence of aneuploidy involving one or more chromosomes have been commonly reported in human tumors. Although these observations were initially made using classic cytogenetic techniques late in a tumor's evolution and were difficult to correlate with cancer progression, more recent studies have reported association of specific nonrandom chromosome aneuploidy with different biologic properties such as loss of hormone dependence and metastatic potential [5].

Classic cytogenetic studies performed on tumor cells had serious limitations in scope because they were applicable only to those cases in which mitotic chromosomes could be obtained. Because of low spontaneous rates of cell division in primary tumors, analyses depended on cells either derived selectively from advanced metastases or those grown *in vitro* for variable periods of time. In both instances, metaphases analyzed represented only a subset of primary tumor cell population. Two major advances in cytogenetic analytic techniques, *in situ* hybridization (ISH) and comparative genomic hybridization (CGH), have allowed better resolution of chromosomal aberrations in freshly isolated tumor cells [6]. ISH analyses with chromosome-specific DNA probes, a powerful adjunct to metaphasic analysis, allows assessment of chromosomal anomalies within tumor cell populations in the contexts of whole nuclear architecture and tissue organization. CGH allows genome wide screening of chromosomal anomalies without the use of specific probes even in the absence of prior knowledge of chromosomes involved. Although both techniques have certain limitations in terms of their resolution power, they nonetheless provide a better approximation of chromosomal changes occurring among tumors of various histology, grade, and stage

compared with what was possible with the classic cytogenetic techniques. Genomic ploidy measurements have also been performed at the DNA level with flow cytometry and cytofluorometric methods. Although these assays underestimate chromosome ploidy due to a chromosomal gain occasionally masking a chromosomal loss in the same cell, several studies using these methods have supported the conclusion that DNA aneuploidy closely associates with poor prognosis in various cancers [7,8]. This discussion of some recent examples published on aneuploidy in cancer includes discussion of studies dealing with DNA ploidy measurements as well. Most of these observations are correlative without direct proof of specific involvement of genes on the respective chromosomes. Identification of putative oncogenes and tumor suppressor genes on gained and lost chromosomes in aneuploid tumors, however, are providing strong evidence that chromosomes involved in aneuploidy play a critical role in the tumorigenic process.

In renal tumors, either segmental or whole chromosome aneuploidy appears to be uniquely associated with specific histologic subtypes [9]. Tumors from patients with hereditary papillary renal carcinomas (HPRC) commonly show trisomy of chromosome 7, when analyzed by CGH. Germline mutations of a putative oncogene *MET* have been detected in patients with HPRC. A recent study [10] has demonstrated that an extra copy of chromosome 7 results in nonrandom duplication of the mutant *MET* allele in HPRC, thereby implicating this trisomy in tumorigenesis. The study suggested that mutation of *MET* may render the cells more susceptible to errors in chromosome replication, and that clonal expansion of cells harboring duplicated chromosome 7 reflects their proliferative advantage. In addition to chromosome 7, trisomy of chromosome 17 in papillary tumors and also of chromosome 8 in mesoblastic nephroma are commonly seen. Association of specific chromosome imbalances with benign and malignant forms of papillary renal tumors, therefore, not only contribute to an understanding of tumor origins and evolution, but also implicate aneuploidy of the respective chromosomes in the tumorigenic transformation process.

In colorectal tumors, chromosome aneuploidy is a common occurrence. In fact, molecular allelotyping studies have suggested that limited karyotyping data available from these tumors actually underestimate the true extent of these changes. Losses of heterozygosity reflecting loss of the maternal or paternal allele in tumors are widespread and often accompanied by a gain of the opposite allele. Therefore, for example, a tumor could lose a maternal chromosome while duplicating the same paternal chromosome, leaving the tumor cell

with a normal karyotype and ploidy but an aberrant allelotype. It has been estimated that cancer of the colon, breast, pancreas, or prostate may lose an average of 25% of its alleles. It is not unusual to discover that a tumor has lost over half of its alleles [4]. In clinical settings, DNA ploidy measurements have revealed that DNA aneuploidy indicates high risk of developing severe premalignant changes in patients with ulcerative colitis, who are known to have an increased risk of developing colorectal cancer [11]. DNA aneuploidy has been found to be one of the useful indicators of lymph node metastasis in patients with gastric carcinoma and associated with poor outcome compared with diploid cases [12,13]. CGH analyses of chromosome aneuploidy, on the other hand, was reported to correlate gain of chromosome 20q with high tumor S phase fractions and loss of 4q with low tumor apoptotic indices [14]. Aneuploidy of chromosome 4 in metastatic colorectal cancer has recently been confirmed in studies that used unbiased DNA fingerprinting with arbitrarily primed polymerase chain reactions to detect moderate gains and losses of specific chromosomal DNA sequences [15]. The molecular karyotype (amplotype) generated from colorectal cancer revealed that moderate gains of sequences from chromosomes 8 and 13 occurred in most tumors, suggesting that overrepresentation of these chromosomal regions is a critical step for metastatic colorectal cancer.

In addition to being implicated in tumorigenesis and correlated with distinct tumor phenotypes, chromosome aneuploidy has been used as a marker of risk assessment and prognosis in several other cancers. The potential value of aneuploidy as a noninvasive tool to identify individuals at high risk of developing head and neck cancer appears especially promising. Interphase fluorescence *in situ* hybridization (FISH) revealed extensive aneuploidy in tumors from patients with head and neck squamous cell carcinomas (HNSCC) and also in clinically normal distant oral regions from the same individuals [16,17]. It has been proposed that a panel of chromosome probes in FISH analyses may serve as an important tool to detect subclinical tumorigenesis and for diagnosis of residual disease. The presence of aneuploid or tetraploid populations is seen in 90% to 95% of esophageal adenocarcinomas, and when seen in conjunction with Barrett's esophagus, a premalignant condition, predicts progression of disease [18,19]. Chromosome ploidy analyses in conjunction with loss of heterozygosity and gene mutation studies in Barrett's esophagus reflect evolution of neoplastic cell lineages *in vivo* [20]. Evolution of neoplastic progeny from Barrett's esophagus following somatic genetic mutations frequently involves bifurcations and loss of heterozygosity at several chromosomal loci leading to aneuploidy and cancer. Accordingly, it is hypothesized that during

tumor cell evolution diploid cell progenitors with somatic genetic abnormalities undergo expansion with acquired genetic instability. Such instability, often manifested in the form of increased incidence of aneuploidy, enters a phase of clonal evolution beginning in premalignant cells that proceeds over a period of time and occasionally leads to malignant transformation. The clonal evolution continues even after the emergence of cancer.

The significance of DNA and chromosome aneuploidy in other human cancers continue to be evaluated. Among papillary thyroid carcinomas, aneuploid DNA content in tumor cells was reported to correlate with distant metastases, reflecting worsened prognosis [21]. Genome wide screening of follicular thyroid tumors by CGH, on the other hand, revealed frequent loss of chromosome 22 in widely invasive follicular carcinomas [22]. Chromosome copy number gains in invasive neoplasm compared with foci of ductal carcinoma *in situ* (DCIS) with similar histology have been proposed to indicate involvement of aneuploidy in progression of human breast cancer [23]. ISH analyses of cervical intraepithelial neoplasia has provided suggestive evidence that chromosomes 1, 7 and X aneusomy is associated with progression toward cervical carcinoma [24].

Although the prognostic value of numeric aberrations remains a matter of debate in human hematopoietic neoplasia, there have been recent studies to suggest that the presence of monosomy 7 defines a distinct subgroup of acute myeloid leukemia patients [25]. It is interesting in this context that therapy-related myelodysplastic syndromes have been reported to display monosomy 5 and 7 karyotypes, reflecting poor prognosis [26].

The clinical observations, mentioned previously, are supported by *in vitro* studies in human and rodent cells in which aneuploidy is induced at early stages of transformation [27,28]. It is even suggested that aneuploidy may cause cell immortalization, in some instances, that is a critical step preceeding transformation.

Finally, in an interesting study to develop transgenic mouse models of human chromosomal diseases, chromosome segment specific duplication and deletions of the genome were reported to be constructed in mouse embryonic stem cells [29]. Three duplications for a portion of mouse chromosome 11 syntenic with human chromosome 17 were established in the mouse germline. Mice with 1Mb duplication developed corneal hyperplasia and thymic tumors. The findings represent the first transgenic mouse model of aneuploidy of a defined chromosome segment that documents the direct role of chromosome aneusomy in tumorigenesis.

Aneuploidy as "dynamic cancer-causing mutation" instead of a "consequential state" in cancer

According to the hypothesis previously discussed, aneuploidy represents either a "gain of function" or "loss of function" mutation at the chromosome level with a causative influence on the tumorigenesis process. The hypothesis, however, is based only on circumstantial evidence even though existence of aneuploidy is correlated with different tumor phenotypes. The existence of numeric chromosomal alterations in a tumor does not mean that the change arose as a dynamic mutation due to genomic instability, because several factors could lead to consequential aneuploidy in tumors, also. Although aneuploidy as a dynamic mutation due to genomic instability in tumor cells would occur at a certain measurable rate per cell generation, a consequential state of aneuploidy in tumors may not occur at a predictable rate under similar conditions or in tumors with similar phenotypes. In addition to genomic instability, differences in environmental factors with selective pressure, could explain high incidence of aneuploidy and other somatic mutations in tumors compared with normal cells [4]. These include humoral, cell substratum, and cell-cell interaction differences between tumor and normal cell environments. It could be argued that despite similar rates of spontaneous aneuploidy induction in normal and tumor cells, the latter are selected to proliferate due to altered selective pressure in the tumor cell environment, whereas the normal cells are eliminated through activation of apoptosis. Alternatively, of course, one could postulate that selective expression or overexpression of anti-apoptotic proteins or inactivation of proapoptotic proteins in tumor cells may counteract default induction of apoptosis in G2/M phase cells undergoing missegregation of chromosomes. Recent demonstration of overexpression of a G2/M phase anti-apoptotic protein survivin in cancer cells [30] suggests that this protein may favor aberrant progression of aneuploid transformed cells through mitosis. This would then lead to proliferation of aneuploid cell lineages, which may undergo clonal evolution.

To ascertain that aneuploidy is a dynamic mutational event, various human tumor cell lines and transformed rodent cell lines have been analyzed for the rate of aneuploidy induction. When grown under controlled *in vitro* conditions, such conditions ensure that environmental factors do not influence selective proliferation of cells with chromosome instability. In one study, Lengauer *et al.* [31•] provided unequivocal evidence by FISH analyses that losses or gains of multiple chromosomes occurred in excess of 10^{-2} per chromosome per generation in aneuploid colorectal cancer cell lines. The study further concluded that such chromosomal instability appeared to be a dominant trait. Using another *in*

vitro model system of Chinese hamster embryo (CHE) cells, Duesberg *et al.* [32•] have also obtained similar results. With clonal cultures of CHE cells, transformed with nongenotoxic chemicals and a mitotic inhibitor, these authors demonstrated that the overwhelming majority of the transformed colonies contained more than 50% aneuploid cells, indicating that aneuploidy would have originated from the same cells that underwent transformation. All the transformed colonies tested were tumorigenic. It was further documented that the ploidy factor representing the quotient of the modal chromosome number divided by the normal diploid number, in each clone, correlated directly with the degree of chromosomal instability. Therefore, chromosomal instability was found proportional to the degree of aneuploidy in the transformed cells and the authors hypothesized that aneuploidy is a unique mechanism of simultaneously altering and destabilizing, in a massive manner, the normal cellular phenotypes. In the absence of any evidence that the transforming chemicals used in the study did not induce other somatic mutations, it is difficult to rule out the contribution of such mutations in the transformation process. These results nonetheless make a strong case for aneuploidy being a dynamic chromosome mutation event intimately associated with cancer.

Aneuploidy versus somatic gene mutation in cancer

The idea that numeric chromosome imbalance or aneuploidy is a direct cause of cancer was proposed at the turn of the century by Theodore Boveri [33]. However, the hypothesis was largely ignored over the last several decades in favor of the somatic gene mutation hypothesis, mentioned earlier. Evidence accumulating in the literature lately on specific chromosome aneusomies recognized in primary tumors, incidence of aneuploidy in cells undergoing transformation, and aneuploid tumor cells showing a high rate of chromosome instability have led to the rejuvenation of Boveri's hypothesis. The concept has recently been discussed as a "vintage wine in a new bottle" [34•]. The author points out that except for rare cancers caused by dominant retroviral oncogenes, diploidy does not seem to occur in solid tumors, whereas aneuploidy is a rule rather than exception in cancer.

Aneuploidy as an effective mutagenic mechanism driving tumor progression, on the other hand, is being recognized as a viable solution to the paradox that with known mutation rate in non-germline cells ($\sim 10^{-7}$ per gene per cell generation) tumor cell lineages cannot accumulate enough mutant genes during a human lifetime [35]. The concept is gaining significant credibility since genes that potentially affect chromosome segregation were found mutated in human cancer. Some of

these genes have also been shown to have transforming capability in *in vitro* assays. Selected recent publications describing the findings are being discussed below in reference to the mitotic targets potentially involved in inducing chromosome segregation anomalies in cells.

Potential mitotic targets and molecular mechanisms of aneuploidy

Because aneuploidy represents numeric imbalance in chromosomes, it is reasonable to expect that aneuploidy arises due to missegregation of chromosomes during cell division. There are many potential mitotic targets, which could cause unequal segregation of chromosomes (Fig. 1). Recent investigations have identified several genes involved in regulating these mitotic targets and mitotic checkpoint functions, which can be implicated in induction of aneuploidy in tumor cells. This discussion is restricted to those mitotic targets and checkpoint genes whose abnormal functioning has been observed in cancer or has been shown to cause tumorigenic transformation of cells, in recent years. The role of telomeres is discussed elsewhere in this issue. For a more detailed description of the components of mitotic machinery and their possible involvement in causing chromosome segregation abnormalities in tumor cells, readers may refer to a recently published review [36•].

Among the mitotic targets implicated in cancer, centrosome defects have been observed in a wide variety of malignant human tumors. Centrosomes play a central role in organizing the microtubule network in interphase cells and mitotic spindle during cell division. Multipolar mitotic spindles have been observed in human cancers *in situ* and abnormalities in the form of supernumerary

centrosomes, centrosomes of aberrant size and shape as well as aberrant phosphorylation of centrosome proteins have been reported in prostate, colon, brain, and breast tumors [37,38]. In view of the findings that abnormal centrosomes retain the ability to nucleate microtubules *in vitro*, it is conceivable that cells with abnormal centrosomes may missegregate chromosomes producing aneuploid cells. The molecular and genetic bases of abnormal centrosome generation and the precise pathway through which they regulate the chromosome segregation process remain to be elucidated. Recent discovery of a centrosome-associated kinase STK15/BTAK/aurora2, naturally amplified and overexpressed in human cancers, has raised the interesting possibility that aberrant expression of this kinase is critically involved in abnormal centrosome function and unequal chromosome segregation in tumor cells [39,40]. Exogenous expression of the kinase in rodent and human cells was found to correlate with an abnormal number of centrosomes, unequal partitioning of chromosomes during division, and tumorigenic transformation of cells. It is relevant in this context to mention that the *Xenopus* homologue of human STK15/BTAK/aurora2 kinase has recently been shown to phosphorylate a microtubule motor protein XIEg5, the human orthologue of which is known to participate in the centrosome separation during mitosis [41]. Findings on STK15/aurora2 kinase, thus, provide an interesting lead to a possible molecular mechanism of centrosome's role in oncogenesis. Centrosomes have, of late, been implicated in oncogenesis from studies revealing supernumerary centrosomes in *p53*-deficient fibroblasts and overexpression of another centrosome kinase PLK1 being detected in human non-small cell lung cancer [42].

One of the critical events that ensures equal partitioning of the chromosomes during mitosis is the proper and timely separation of sister chromatids that are attached to each other and to the mitotic spindle. Untimely separation of sister chromatids has been suspected as a cause of aneuploidy in human tumors. Cohesion between sister chromatids is established during replication of chromosomes and is retained until the next metaphase/anaphase transition. It has been shown that during metaphase-anaphase transition, the anaphase promoting complex/cyclosome triggers the degradation of a group of proteins called securins that inhibit sister chromatid separation. A vertebrate securin (*v*-securin) has recently been identified that inhibits sister chromatid separation and is involved in transformation and tumorigenesis. Subsequent analysis revealed that the human securin is identical to the product of the gene called pituitary tumor transforming gene, which is overexpressed in some tumors and exhibits transforming activity in NIH3T3 cells. It is proposed that elevated expression of the *v*-securin may contribute to generation of malignant tumors due to

Figure 1. Potential mitotic targets causing aneuploidy in oncogenesis

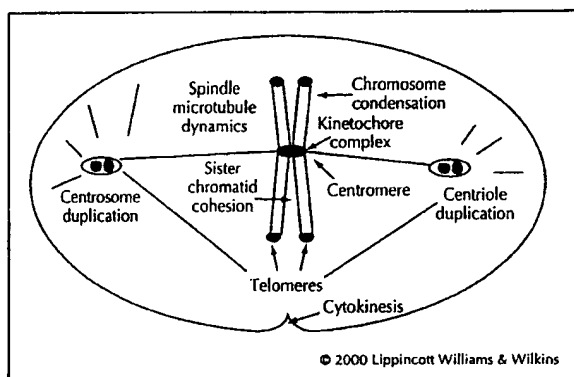


Diagram illustrates that defects in several processes involving chromosomal, spindle microtubule, and centrosomal targets, in addition to abnormal cytokinesis, may cause unequal partitioning of chromosomes during mitosis, leading to aneuploidy. Recently obtained evidence in favor of some of these possibilities is discussed in the text.

chromosome gain or loss produced by errors in chromatid separation [43•].

Normal progression through mitosis during prophase to anaphase transition is monitored at least at two checkpoints. One checkpoint operates during early prophase at G2 to metaphase progression while the second ensures proper segregation of chromosomes during metaphase to anaphase transition. Several mitotic checkpoint genes responding to mitotic spindle defects have been identified in yeast. The metaphase-anaphase transition is delayed following activation of this checkpoint during which kinetochores remain unattached to the spindle. The signal is transmitted through a kinetochore protein complex consisting of Mps1p and several Mad and Bub proteins [44]. It is expected that for unequal chromosome segregation to be perpetuated through cell proliferation cycles giving rise to aneuploidy, checkpoint controls have to be abrogated.

Following this logic, Vogelstein *et al.* [45•] hypothesized that aneuploid tumors would reveal mutation in mitotic spindle checkpoint genes. Subsequent studies by these investigators have proven the validity of this hypothesis and a small fraction of human colorectal cancers have revealed the presence of mutations in either hBub1 or hBubR1 checkpoint genes. It was further revealed that mutant BUB1 could function in a dominant negative manner conferring an abnormal spindle checkpoint when expressed exogenously. Inactivation of spindle checkpoint function in virally induced leukemia has also recently been documented following the finding that hMAD1 checkpoint protein is targeted by the Tax protein of the human T-cell leukemia virus type 1. Abrogation of hMAD1 function leads to multinucleation and aneuploidy [46].

In addition to mitotic spindle checkpoint defects, failed DNA damage checkpoint function in yeast is frequently associated with aberrant chromosome segregation as well. It, therefore, appears intriguing yet relevant that the human *BRCA1* gene, proposed to be involved in DNA damage checkpoint function, when mutated by a targeted deletion of exon 11 led to defective G2/M cell cycle checkpoint function and genetic instability in mouse embryonic fibroblasts [47]. The cells revealed multiple functional centrosomes and unequal chromosome segregation and aneuploidy. Although the molecular basis for these abnormalities is not known at this time, it raises the interesting possibility that such an aneuploidy-driven mechanism may be involved in tumorigenesis in individuals carrying germline mutations of *BRCA1* gene.

Conclusion

Growing evidence from human tumor cytogenetic investigations strongly suggest that aneuploidy is associated with the development of tumor phenotypes. Clinical findings of correlation between aneuploidy and tumorigenesis are supported by studies with *in vitro* grown transformed cell lines. Molecular genetic analyses of tumor cells provide credible evidence that mutations in genes controlling chromosome segregation during mitosis play a critical role in causing chromosome instability leading to aneuploidy in cancer. Further elucidation of molecular and physiologic bases of chromosome instability and aneuploidy induction could lead to the development of new therapeutic approaches for common forms of cancer.

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Analysis of Genomic and Proteomic Data Using Advanced Literature Mining

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High-throughput technologies, such as proteomic screening and DNA micro-arrays, produce vast amounts of data requiring comprehensive analytical methods to decipher the biologically relevant results. One approach would be to manually search the biomedical literature; however, this would be an arduous task. We developed an automated literature-mining tool, termed MedGene, which comprehensively summarizes and estimates the relative strengths of all human gene-disease relationships in Medline. Using MedGene, we analyzed a novel micro-array expression dataset comparing breast cancer and normal breast tissue in the context of existing knowledge. We found no correlation between the strength of the literature association and the magnitude of the difference in expression level when considering changes as high as 5-fold; however, a significant correlation was observed ($r = 0.41$; $p = 0.05$) among genes showing an expression difference of 10-fold or more. Interestingly, this only held true for estrogen receptor (ER) positive tumors, not ER negative. MedGene identified a set of relatively understudied, yet highly expressed genes in ER negative tumors worthy of further examination.

Keywords: bioinformatics • micro-array • text mining • gene-disease association • breast cancer

Introduction

At its current pace, the accumulation of biomedical literature outpaces the ability of most researchers and clinicians to stay abreast of their own immediate fields, let alone cover a broader range of topics. For example, to follow a single disease, e.g., breast cancer, a researcher would have had to scan 130 different journals and read 27 papers per day in 1999.¹ This problem is accentuated with high-throughput technologies such as DNA micro-arrays and proteomics, which require the analysis of large datasets involving thousands of genes, many of which are unfamiliar to a particular researcher. In any microarray experiment, thousands of genes may demonstrate statistically significant expression changes, but only a fraction of these may be relevant to the study. The ability to interpret these datasets would be enhanced if they could be compared to a comprehensive summary of what is known about all genes. Thus, there is a need to summarize existing knowledge in a format that allows for the rapid analysis of associations between genes and diseases or other specific biological concepts.

One solution to this problem is to compile structured digital resources, such as the Breast Cancer Gene Database² and the Tumor Gene Database.³ However, as these resources are hand-curated, the labor-intensive review process becomes a rate-limiting step in the growth of the database. As a result, these

databases have a limited scale and the genes are not selected in a systematic fashion.

An alternative approach is automated text mining; a method which involves automated information extraction by searching documents for text strings and analyzing their frequency and context. This approach has been used successfully in several instances for biological applications. In most cases, it has been applied to extract information about the relationships or interactions that proteins or genes have with one another, in the literature or by functional annotation.⁴⁻⁷ Thus far, few publications have applied text-mining to examine the global relationships between genes and diseases. Perez-Iratxeta et al. automatically examined the GO (Gene Ontology) annotation of genes and their predicted chromosomal locations in order to identify genes linked to inherited disorders.⁸

To obtain a more global understanding of disease development, it would be valuable to incorporate information regarding all possible gene-disease relationships, including biochemical, physiological, pharmacological, epidemiological, as well as genetic. This information would enable comprehensive comparisons between large experimental datasets and existing knowledge in the literature. This would accomplish two things. First, it would serve to validate experiments by demonstrating that known responses occur as predicted. Second, it would rapidly highlight which genes are corroborated by the literature and which genes are novel in a given context. We have utilized a computational approach to literature mining to produce a

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comprehensive set of gene-disease relationships. In addition, we have developed a novel approach to assess the strength of each association based on the frequency of citation and co-citation. We applied this tool to help interpret the data from a large micro-array gene expression experiment comparing normal and cancerous breast tissue.

Methods

MedGene Database. MedGene is a relational database, storing disease and gene information from NCBI, text mining results, statistical scores, and hyperlinks to the primary literature. MedGene has a web-based user interface for users to query the database (<http://hipseq.med.harvard.edu/MedGene/>).

Text Mining Algorithms. MeSH files were downloaded from the MeSH web site at NLM (National Library of Medicine) (<http://www.nlm.nih.gov/mesh/meshhome.html>) and human disease categories were selected. LocusLink files were downloaded from the LocusLink web site at NCBI (<http://www.ncbi.nlm.gov/LocusLink/>). Official/preferred gene symbol, official/preferred gene name, and gene alternative symbols and names, all relevant annotations and URLs for each LocusLink record, were collected. Gene search terms were used for literature searching and included all qualified gene names, gene symbols, and gene family terms. Primary gene keys, predominantly qualified gene family terms and gene official/preferred symbols, were used to index Medline records. If the official/preferred gene symbols did not meet the standards to be an index, then qualified gene official/preferred names were used. A local copy of Medline records (up to July, 2002) was pre-selected.

A JAVA module examined the MeSH terms and then indexed each Medline record with the appropriate disease terms. A separate JAVA module was used to examine the titles and abstracts for gene search terms and then to index the gene-related Medline records with the relevant primary gene key(s).

Statistical Methods. For every gene and disease pair, we counted records that were indexed for both gene and disease (double positive hits), for disease only (disease single hits), for gene only (gene single hits), and for neither gene nor disease (double negative hits) to generate a 2×2 contingency table. On the basis of the contingency table-framework, we applied different statistical methods to estimate the strength of gene-disease relationships and evaluated the results. These methods included chi-square analysis, Fisher's exact probabilities, relative risk of gene, and relative risk of disease¹⁶ (<http://hipseq.med.harvard.edu/MedGene/>). In addition, we computed the "product of frequency", which is the product of the proportion of disease/gene double hits to disease single hits and the proportion of disease/gene double hits to gene single hits. To obtain a normal distribution, we transformed all the statistical scores using the natural logarithm. We selected the log of the product of frequency (LPF) to validate MedGene and to use for the analysis with the micro-array data. Spearman rank-correlation coefficients were used to assess the linear relationship between LPF and micro-array fold change in expression level.

Global Analysis. Diseases with at least 50 related genes were selected for clustering analysis, and the LPF scores were normalized with total score for each disease. Hierarchical clustering was done with the "Cluster" software and the clustering result was visualized using "TreeView" (<http://rana.lbl.gov/EisenSoftware.htm>).

Breast Tissue Micro-Arrays. Eighty-nine breast cancer samples (79% ER-positive) and 7 normal breast tissue samples were selected from the Harvard Breast SPORE frozen tissue repository and were representative of the spectrum of histological types, grades, and hormone receptor immuno-phenotypes of breast cancer. Biotinylated cRNA, generated from the total RNA extracted from the bulk tumor, was hybridized to Affymetrix U95A oligo-nucleotide micro-arrays. These micro-arrays consist of 12 400 probes, which represent approximately 9000 genes. Raw expression values were obtained using GENE-CHIP software from Affymetrix, and then further analyzed using the DNA-Chip Analyzer (dChip) custom software.

Results

Automated Indexing of Medline Records by Disease and Gene. To study the gene-disease associations in the literature, we first compiled complete lists for human diseases and human genes. To index all Medline records that were relevant to human diseases, the Medical Subject Heading (MeSH) index of Medline records was utilized. MeSH is a controlled medical vocabulary from the National Library of Medicine and consists of a set of terms or subject headings that are arranged in both an alphabetic and an hierarchical structure. Medline records are reviewed manually and MeSH terms are added to each with software assistance.^{9,10} Twenty-three human disease category headings along with all of their child terms (see the Supporting Information, Supplemental Table 1, or visit http://hipseq.med.harvard.edu/MedGene/publication/s_Table1.html) were selected from the 2002 MeSH index creating a list of 4033 human diseases.

No index comparable to the MeSH Index exists for genes, and thus, it was necessary to apply a string search algorithm for gene names or symbols found in Medline text. A complete list of genes, gene names, gene symbols, and frequently used synonyms were collected from the LocusLink database at NCBI,^{11,12} which contains 53 259 independent records keyed by an official gene symbol or name (June 18th, 2002). For the purposes of this study, no distinction was made between genes and their gene products. Authors often use the same name for both, differentiating the two only by the use of italics, if at all. For the intended use of this study, this lack of distinction is unlikely to have a large effect and may in fact be beneficial.

Initial attempts to search the literature using these lists revealed several sources of false positives and false negatives (Table 1). False positives primarily arose when the searched term had other meanings, whereas false negatives arose from syntax discrepancies necessitating the development of filters to reduce these errors. The syntax issues were readily handled by including alternate syntax forms in the search terms. The false positive cases, caused by duplicative and unrelated meanings for the terms, were more difficult to manage. Where possible, case sensitive string mapping reduced inappropriate citations. In many cases, however, this was not sufficient and the terms had to be eliminated entirely, thereby reducing the false positive rate but unavoidably under-representing some genes.

For the purposes of data tracking, a primary gene key was selected to represent all synonyms that correspond to each gene. Medline records were indexed with a primary gene key when any synonym for that key was found in the title or abstract. Case-insensitive string mapping was used for all searches except as noted above. No additional weight was

Table 1. Systematic Sources of False Positives and False Negatives in Unfiltered Data*

source of error	error type	example	filter solution
gene symbol/name is not unique	false positive	MAG—myelin associated glycoprotein MAG—malignancy-associated protein	eliminate this term
gene symbol is unrelated abbreviation	false positive	PA—pallid homologue (mouse), pallidin (also abbrev. for Pennsylvania)	eliminate this term
gene symbol/name has language meaning	false positive	WAS—Wiskott—Aldrich Syndrome (also the word "was")	case-sensitive string search
nonstandard syntax	false negative	BAG-1 instead of BAG1	add dash term
unofficial gene name/symbol	false negative	P53 instead of TP53	add all gene nicknames
nonspecified gene name	false negative	estrogen receptor instead of Estrogen receptor 1	add family stem term

* In preliminary studies, Medline was searched for co-occurrence of genes and diseases and the resulting output was evaluated to identify error sources that were amenable to global filters. Each error source is categorized by the type of error it causes: false positives are suggested relationships that are not real and false negatives are real relationships that are underrepresented. The filter solutions used are indicated. Note that in some cases, the filter solution itself introduces error. In general, error rates maximized sensitivity, even at the expense of specificity if needed.

added for multiple occurrences of a term or the co-occurrence of multiple synonyms for the same gene key.

Medline records were searched with all qualified gene identifiers, such as the official/preferred gene symbol, the official/preferred gene name, all gene nicknames and all syntax variants. In situations where there are several members of a gene family or splice variants, some authors prefer to use a shortened gene family name, e.g., estrogen receptor instead of estrogen receptor 1 (*ESR1*), creating a source of false negatives. For this reason, gene family stem terms were created for all genes that have an alpha or numerical suffix (e.g., *IL2RA*, *TGFB*, *ESR1*, etc.) and then used to search the literature. The family stem terms were handled separately from the specific gene names so that it would be clear when linkages were made to the gene family versus a specific member in that family.

To improve performance and accuracy, some pre-selection was applied to the records that were scanned. First, review articles were eliminated to avoid redundant treatment of citations. Second, non-English journals were removed because the natural language filters were only relevant to English publications. Finally, journals unlikely to contain primary data about gene-disease relationships were also removed (e.g., *Int. J. Health Educ.*, *Bedside Nurse*, and *J. Health Econ.*). Together, these filters reduced the 12 198 221 Medline publications (July 2002) by 37%.

Ranking the Relative Strengths of Gene-Disease Associations. In total, there were 618 708 gene-disease co-citations, in which 16% (8297) of all studied genes had been associated to a disease and 96% (3875) of all diseases had been associated to at least one gene. To rank the relative strengths of gene disease relationships, we tested several different statistical methods and examined the results. With the exception of the relative risk estimates, the methods provided similar results with respect to the rank order of the gene-disease association strengths. However, after comparing the results to other databases and after consulting disease experts, the log of the product of frequency (LPF) was selected for further analysis because it gave the best results overall.

Validation of MedGene. In developing this tool, it was important to minimize the number of missed genes (false negatives) and misclassified genes (false positives). However, in situations when these goals were in conflict, inclusiveness was prioritized. To determine the false negative rate in MedGene, breast cancer was used as a test case because it was associated with more genes than any other human disease and because

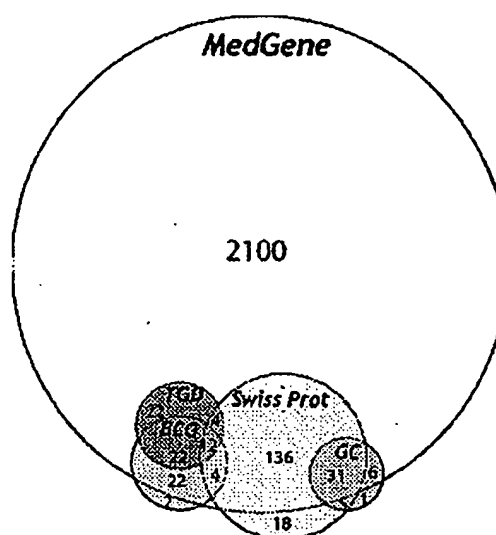


Figure 1. Estimation of the false negative rate by comparison with hand-curated databases. The breast cancer-related genes identified by MedGene were compared with those listed in several other databases including the Tumor Gene Database (TGD),² the Breast Cancer Gene Database (BCG),¹ GeneCards (GC)¹⁷ and Swissprot.¹⁸ Genes were considered false negatives if they were represented in at least one of these other databases and not in MedGene and their link to breast cancer was supported by at least one literature reference. All literature references were verified by manual review to confirm their validity. The number of genes in each database or shared by more than one database is indicated. The false negative rate was calculated by genes missed at MedGene (26)/total number of nonoverlapping genes in other databases (285).

there were several public databases that link genes to breast cancer. We compared the list of breast cancer-related genes from MedGene to these databases, illustrated in Figure 1. Among the 285 distinct breast cancer-related genes that were supported by at least one literature citation in these hand-curated databases, 26 were absent from MedGene, suggesting a false negative rate of approximately 9%. To determine why these were missed, all literature references for these genes (80

papers) were reviewed manually (see the Supporting Information, Supplemental Table 2, or visit http://hipseq.med.harvard.edu/MedGene/publication/s_Table_2.html). Among these papers, most false negatives were caused by nonstandard gene terms or gene terms eliminated by our specificity filters. Few genes were missed because they were only mentioned in review papers (0.4%) or they appeared only in the body of the manuscript but not the abstract or title (1.1%). Of note, MedGene identified approximately 2000 additional breast cancer-related genes not listed in any other database.

To assess the false positive error rate, two complementary approaches were used: a detailed analysis of one disease and a global examination of 1000 diseases. The detailed approach examined the false positive error rate and its sources, whereas the global approach tested whether the overall results made biomedical sense.

Using the LPF, 1467 genes related to prostate cancer were assembled in rank order. We then retrieved approximately 300 Medline records each for the highest ranked 100 and the lowest ranked 200 genes and manually reviewed the titles and abstracts to determine the verity of the association. Nearly 80% of the highest ranked 100 genes fell into one of the five categories that reflect meaningful gene-disease relationships (see the Supporting Information, Supplemental Table 3, or visit http://hipseq.med.harvard.edu/MedGene/publication/s_Table_3.html). Among the lowest ranked 200 genes, approximately 70% reflected true relationships. Of the 600 records reviewed, there were only two in which the association between the gene and the disease was described as negative. Both were genes with very low scores. In both cases, the authors did not argue the absence of any relationship, but rather that a particular feature of the gene or protein was not shown to be related to human prostate cancer.^{12,14}

The coincidence of some gene symbols with medical abbreviations, chemical abbreviations and biological abbreviations resulted in most of the false positives (see the Supporting Information, Supplemental Table 4, or visit http://hipseq.med.harvard.edu/MedGene/publication/s_Table_4.html), emphasizing the importance of the filters that were added in the search algorithm (Table 1). Without the filters, the false positive rate more than doubled, and the false negative rate rose dramatically (data not shown). For example, among the papers about breast cancer, there were only 12 Medline records that referred to *ESR1* and 10 to *ESR2*, whereas almost 2000 papers mentioned estrogen receptor without specifying *ESR1* or *ESR2*; this latter group was detected by the family stem term filter.

To further validate these results, a global analysis of the gene-disease relationships described by MedGene was performed. For this experiment, it was reasoned that the more closely related the diseases are to one another, the more they will be related to the same gene sets. Thus, if the relationships defined by MedGene accurately reflected the literature, then an unsupervised hierarchical clustering of the gene data should group diseases in a manner consistent with common medical thinking. Conversely, if the clustered diseases do not make sense biologically or medically, it may reflect excessive false positives, false negatives, or inappropriate scoring of the data.

To execute this experiment, the gene sets and the corresponding LPF values for 1000 randomly selected diseases (each with at least 50 gene relationships) were used as a dataset for clustering the diseases. A review of the results showed that the resulting disease clusters were indeed logical based upon common medical knowledge (see the Supporting Information,

Supplemental Figure 1, or visit http://hipseq.med.harvard.edu/MedGene/publication/s_Figure_1.html). For example, in one such cluster shown in Figure 2, diabetes and its complications grouped together and were also closely linked to diseases associated with starvation states.

The number of genes associated with a given disease can be estimated by adjusting the MedGene number up by the false negative rate (~9%) and down by the false positive rate (~26% on average). Using this, the average disease has 103.7 ± 45.3 (mean \pm s.d.) genes associated with it, although the range is quite broad with 2359 genes related to breast cancer, 2122 genes related to lung cancer and no genes related to a number of diseases.

Applying MedGene to the Analysis of Large Datasets. Access to a comprehensive summary of the genes linked to human diseases provided an opportunity to analyze data obtained from a high-throughput experiment. We compared the MedGene breast cancer gene list to a gene expression data set generated from a micro-array analysis comparing breast cancer and normal breast tissue samples. Micro-array analysis identified 2286 genes that had greater than a 1-fold difference in mean expression level between breast cancer samples and normal breast samples. Using MedGene, we sorted the 2286 genes into four classes: 555 genes directly linked to breast cancer in the literature by gene term search (first-degree association by gene name); 328 genes directly linked by family term search (first-degree association by family term); 1021 genes linked to breast cancer only through other breast cancer genes (second-degree association); and 505 genes not previously associated with breast cancer. (See the Supporting Information, Supplemental Figure 2, or visit http://hipseq.med.harvard.edu/MedGene/publication/s_Figure_2.html.) Among the 505 previously unrelated genes, 467 were either newly identified genes or genes that had not previously been associated with any disease. Among the remaining 38 genes, 9 had been related to other cancers, specifically esophageal, colon, uterine, skin, and cervix.

To determine whether the genes highlighted by the micro-array analysis were more likely to have been previously linked to breast cancer in the literature, we created a two-dimensional plot of the fold change of expression level between breast cancer and normal tissue versus the literature score (LPF) (Figure 3A). There was a broad spread of expression changes among the genes directly linked to breast cancer ranging from less than 1-fold change (68%) to over 40-fold (0.3%). Notably, the majority of genes with greater than 10-fold expression changes were linked to breast cancer by first-degree association.

Among all 754 genes directly linked to breast cancer in the literature, there was no correlation between LPF and micro-array fold change ($r = 0.018$, p -value = 0.62). However, when we stratified the analysis based on the magnitude of the fold change, we observed an increasing trend in correlation (Figure 3B) suggesting that genes with a more substantial change in expression level were more likely to have a stronger association in the literature. For genes that had 10-fold change or more in expression level, the correlation increased to 0.41 (p -value = 0.05).

When we evaluated the micro-array data separately for ER positive and ER negative tumors, the trend in correlation between fold change and literature score was highly dependent on estrogen receptor status. Interestingly, there was a similar trend in correlation for ER positive tumors, but no trend in correlation for ER negative tumors.

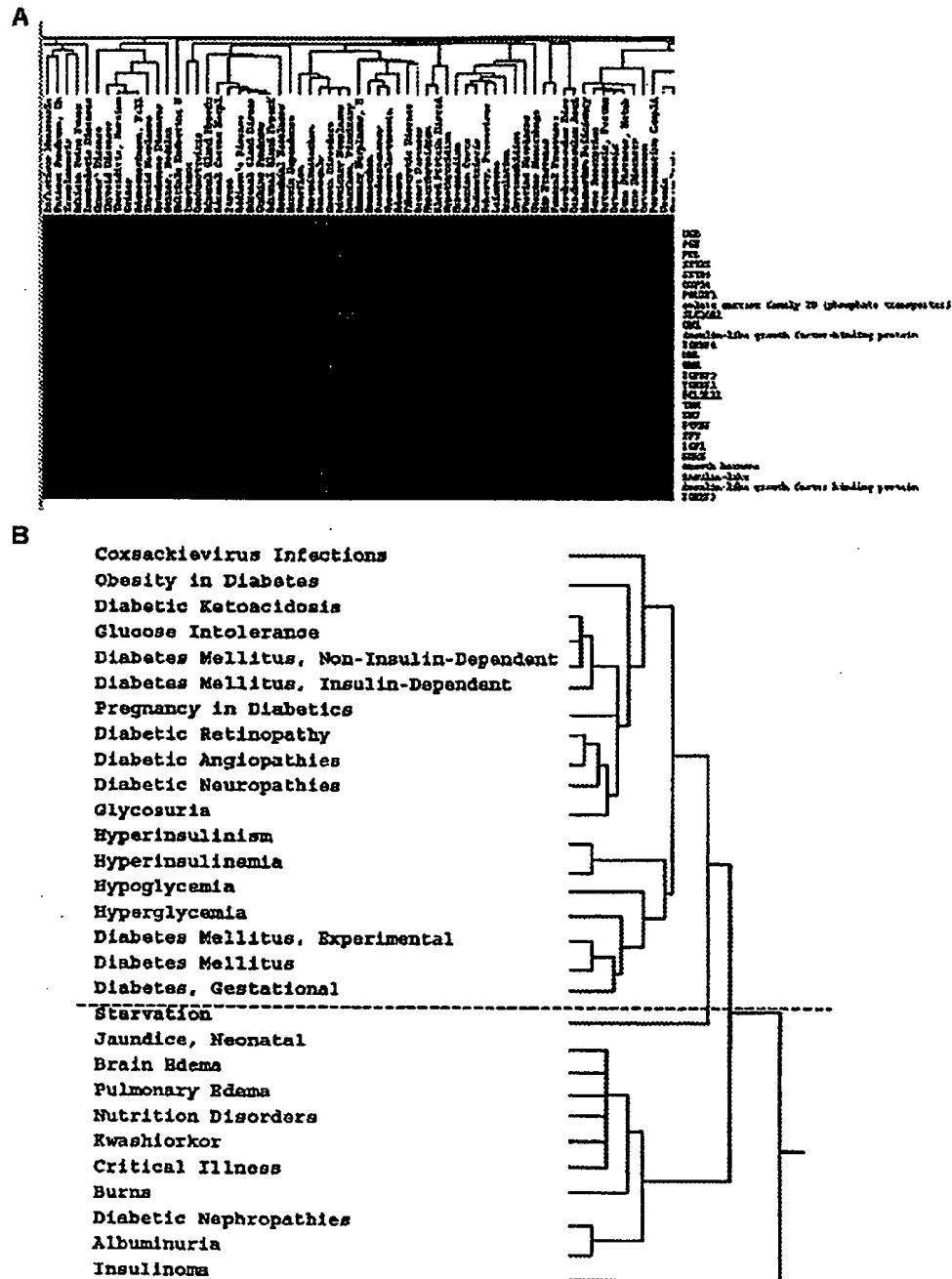


Figure 2. Global validation by clustering analysis. 2(A). The gene sets and the corresponding LPF values for 1000 diseases, each with at least 50 gene relationships, were used in an unsupervised clustering of the diseases based on the gene patterns associated with them. A sample of the data is shown here. 2(B). One of the resulting clusters is shown that corresponds to blood sugar states. Diabetes terms (above the line) and starvation states terms (under the line) clustered together. Within these groups, there is also clustering of diabetic small vessel complications, altered serum chemistries, nutritional disorders, etc. (Supplemental Figure 1: http://hipseq.med.harvard.edu/MedGene/publication/s_Figure1.html).

Finally, to validate our findings, we computed similar correlations between the breast cancer expression data and LPF scores generated by MedGene for hypertension, a

disease unrelated to breast cancer. As expected, we did not observe an increasing trend in correlation for hypertension.

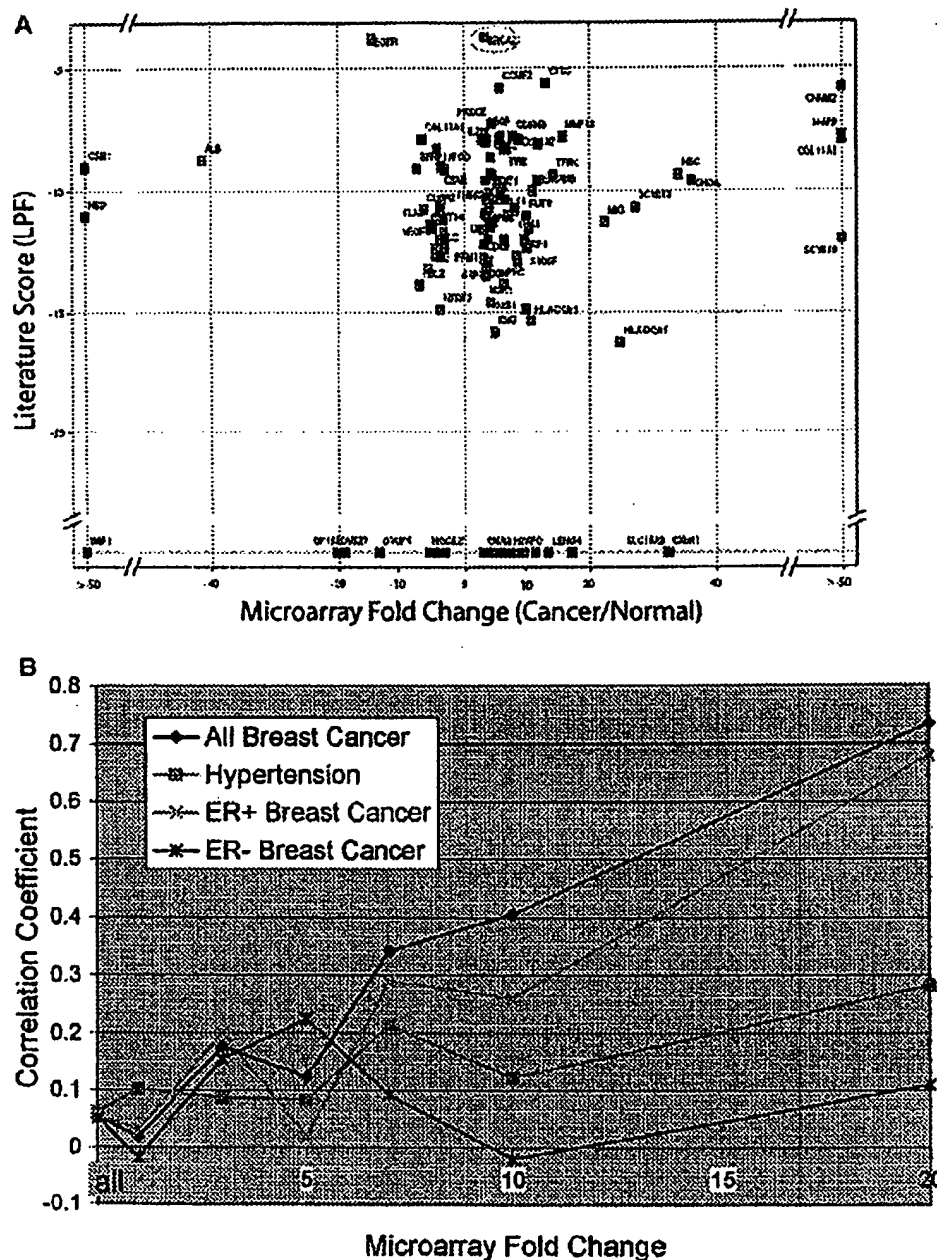


Figure 3. Relationship between literature score and functional data for breast cancer. 3A. The data from an expression analysis of samples for breast tumors and normal breast tissue were analyzed to indicate the fold difference of expression level between breast tumor and normal sample (cutoff ≥ 3 -fold change). The fold changes were plotted against the literature score for the same gene set. Green dots represent first-degree association by gene search, blue dots represent first-degree association by family search and red dots represent no-association. Some well-studied genes, such as BRCA2 (pink circle), are not reflected by a substantial difference in expression level. Furthermore, the majority of genes that have no association with breast cancer in the literature had less than 10-fold expression changes (shaded area). 3B. The Spearman rank-correlation coefficients between literature score (LPF) and the fold change of expression level between tumor and normal breast samples (y-axis) in relation to the amount of fold change of expression level (x-axis). Gene rank lists were generated for breast cancer (blue) and hypertension (pink). Correlations were also computed between the breast cancer gene LPF scores and fold change expression data among estrogen receptor positive tumors only (light blue) and estrogen receptor negative tumors only (purple).

Table 2. Top 25 Genes Related to Selected Human Diseases*

breast neoplasms	hypertension	rheumatoid arthritis	bipolar disorder	atherosclerosis
estrogen receptor	<i>REN</i>	<i>RA</i>	<i>ERDA1</i>	apolipoprotein
<i>PCR</i>	<i>DBP</i>	<i>TNFRSF10A</i>	<i>SNAP29</i>	<i>APOE</i>
<i>ERBB2</i>	<i>LEP</i>	<i>CRP</i>	<i>PFKL</i>	<i>LDLR</i>
<i>BRCA1</i>	<i>AGT</i>	<i>AS</i>	<i>DRD2</i>	<i>ELN</i>
<i>BRCA2</i>	<i>INS</i>	<i>ESR1</i>	<i>TRH</i>	<i>ARG1</i>
<i>EGFR</i>	kallikrein	<i>HLA-DRB1</i>	<i>IMPA2</i>	<i>APOB</i>
<i>CYP19</i>	<i>ACE</i>	<i>DR1</i>	<i>HTR3A</i>	<i>APOA1</i>
<i>TFF1</i>	endothelin	interleukin	<i>DRD3</i>	<i>MSR1</i>
<i>PSEN2</i>	<i>S100A6</i>	<i>TNF</i>	<i>REM</i>	<i>LPL</i>
<i>TP53</i>	<i>BDK</i>	<i>IL6</i>	<i>KCNN3</i>	<i>PON1</i>
<i>CES3</i>	<i>DIANPH</i>	collagen	<i>DRD4</i>	plasminogen
<i>CEACAM5</i>	<i>SAR1</i>	<i>IL1A</i>	<i>HTR2C</i>	activator inhibitor
<i>ERBB3</i>	<i>PIH</i>	<i>ACR</i>	<i>RELN</i>	<i>PLG</i>
cyclin	<i>CD59</i>	<i>TNFRSF12</i>	<i>DBH</i>	vascular cell
<i>COX5A</i>	<i>ALB</i>	<i>IL2</i>	<i>MAOA</i>	adhesion molecule
cathepsin	<i>CYP11B2</i>	<i>CHI3L1</i>	<i>COMT</i>	<i>ATOH1</i>
<i>ERBB4</i>	<i>MAT2B</i>	<i>IL8</i>	<i>HTR2A</i>	<i>VWF</i>
<i>TRAM</i>	angiotensin receptor	interleukin 1 matrix	<i>SYNJ1</i>	<i>INS</i>
<i>CCND1</i>	<i>AGTR2</i>	metalloproteinase	<i>INPP1</i>	<i>ARG2</i>
<i>EGF</i>	<i>NPPA</i>	interferon	<i>NEDD4L</i>	<i>ABCA1</i>
<i>MUC1</i>	<i>LVM</i>	<i>CD68</i>	<i>FRA13C</i>	<i>OLR1</i>
insulin-like	<i>DBH</i>	<i>IL4</i>	transducer of	collagen
<i>BCL2</i>	<i>NPY</i>	<i>IL17</i>	<i>ERBB2</i>	<i>MCP</i>
mucin	<i>POMC</i>	<i>MMP3</i>	<i>BAIAP3</i>	lipoprotein
<i>FGF3</i>	neuropeptide	<i>SIL</i>	<i>ATP1B3</i>	<i>APOA2</i>
			<i>DRD5</i>	intercellular
				adhesion molecule
				<i>RAB27A</i>

* MedGene results for the top 25 genes associated with breast neoplasms, hypertension, rheumatoid arthritis, bipolar disorder, and atherosclerosis, respectively, ranked by LPF scores. The hyperlink to all the papers co-citing the gene and the disease is available at MedGene website (<http://hipseq.med.harvard.edu/MedGene/>).

Discussion

The Human Genome Project heralded a new era in biological research where the emphasis on understanding specific pathways has expanded to global studies of genomic organization and biological systems. High-throughput technologies can provide novel insight into comprehensive biological function but also introduces new challenges. The utility of these technologies is limited to the ability to generate, analyze, and interpret large gene lists. MedGene, a relational database derived by mining the information in Medline, was created to address this need. MedGene users can query for a rank-ordered list of human gene-disease relationships (Table 2) for one or more diseases. Each entry is hyperlinked to the original papers supporting each association and to other relevant databases.

MedGene is an innovative extension of previous text mining approaches. Perez-Irujo et al. used the GO annotation and their chromosomal locations to predict genes that may contribute to inherited disorders.⁴ MedGene takes a broader view and includes all diseases and all possible gene-disease relationships. Furthermore, MedGene utilizes co-citation to indicate a relationship rather than GO annotation, which is limited to the subset of genes that have GO annotation. Our approach is complementary to that taken by Chaussabel and Sher, who used the frequency of co-cited terms to cluster genes into a hierarchy of gene-gene relationships.⁵

A unique aspect of this tool is the ability to assess the relative strengths of gene-disease relationships based on the frequency of both co-citation and single citation. This presupposes that most co-citations describe a positive association, often referred to as publication bias¹⁵ and is supported by our observations

that negative associations are rare (Supplemental Table 3: http://hipseq.med.harvard.edu/MedGene/publication/s_Table3.html). Of course, relationships established by frequency of co-citation do not necessarily represent a true biological link; however, it is strong evidence to support a true relationship.

Another important feature of MedGene is the implementation of software filters that substantially reduced the error rate. We estimate that less than 10% of all associations were missed and at least 70% of even the weakest associations were real. For this study, all of the filters that we applied were general ones, e.g., expanding the list of all gene names to address the different syntax forms used by different journals, eliminating gene names that correspond to common English words, etc. The majority of the remaining search term ambiguities were idiosyncratic and difficult to identify systematically without causing a significant rise in false negatives. Alternative approaches, such as the examination of the nearest neighbor terms, need to be considered to further reduce the false positive rate.

It is not uncommon to see expression changes in microarray experiments as small as 2-fold reported in the literature. Even when these expression changes are statistically significant, it is not always clear if they are biologically meaningful. When comparing expression levels of disease to normal tissue, one expects an enrichment of known disease-related genes to appear in the altered expression group. MedGene provided a unique opportunity to test this notion in the context of existing knowledge on a novel breast cancer microarray dataset. For genes displaying a 5-fold change or less in tumors compared to normal, there was no evidence of a correlation between altered gene expression and a known role in the disease. This

Table 3. Genes with Large Expression Changes in ER- but Not in ER+ Breast Tumors

gene symbol	fold change (ER+)	fold change (ER-)
<i>KRT18B1</i>	1.0	610.8
<i>BRS3</i>	1.2	89.4
<i>DKK1</i>	1.2	69.8
<i>ZIC1</i>	1.9	59.6
<i>TLR1</i>	1.0	38.5
<i>KIAA0680</i>	2.6	33.2
<i>CDKN3</i>	1.0	30.6
<i>EBI2</i>	4.0	27.9
<i>GZMB</i>	3.8	21.9
<i>STK18</i>	4.7	18.6
<i>GPR49</i>	1.0	14.6
<i>MYO10</i>	1.6	14.4
<i>LAD1</i>	-1.0	13.5
<i>POLE2</i>	4.2	13.0
<i>HMG4</i>	4.4	12.9
<i>BCL2L11</i>	-1.2	12.3
<i>LRP8</i>	2.9	12.2
<i>CCNB2</i>	1.0	11.8
<i>CCNE2</i>	4.0	11.6
<i>FCB</i>	-4.3	11.1
<i>KNSL6</i>	2.9	10.9
<i>HIF5</i>	3.0	10.2
<i>SERPINH2</i>	4.6	10.2
<i>YAP1</i>	1.0	10.0
<i>LPHB</i>	-1.3	-10.4
<i>TCEA2</i>	-1.1	-10.8
<i>TFF1</i>	1.3	-11.4
<i>COL17A1</i>	-4.1	-15.7
<i>POP5</i>	1.1	-16.2
<i>BPAG1</i>	-4.6	-22.3
<i>PDZK1</i>	-1.1	-36.8
<i>VEGFC</i>	-2.8	-51.5
<i>MUC6</i>	-1.4	-64.9
<i>SERPINA5</i>	-1.0	-83.1
<i>MEIS1</i>	-1.6	-85.9
<i>CA12</i>	2.4	-150.3

Table 3. MedGene identified a set of relatively understudied, yet highly expressed genes in ER negative, but not ER positive breast tumors. All of these genes have either never been co-cited with breast cancer or have a weak association except those marked with an *.

reflects the many genes whose role in breast cancer may not involve large changes in expression in sporadic tumors (e.g., *BRCA1* and *BRCA2*) and genes whose modest changes in expression may be unrelated to the disease. Strikingly, among genes with a 10-fold change or more in expression level, there was a strong and significant correlation between expression level and a published role in the disease, providing the first global validation of the micro-array approach to identifying disease-specific genes.

The results derived from MedGene have two implications. First, a careful hunt for corroborating evidence of a role in breast cancer should precede any further study of genes with less than 5-fold expression level changes. Second, any genes with 10-fold changes or more are likely to be related to breast cancer and warrant attention. It is likely that this threshold will change depending on the disease as well as the experiment.

Interestingly, the observed correlation was only found among ER-positive tumors, not ER-negative. This may reflect a bias in the literature to study the more prevalent type of tumor in the population. Furthermore, this emphasizes that caution must be taken when interpreting experiments that may contain subpopulations that behave very differently. The MedGene approach identified a set of relatively understudied, yet highly expressed genes in ER-negative tumors that are worthy of further examination (Table 3).

In conclusion, we have developed an automated method of summarizing and organizing the vast biomedical literature. To our knowledge, the resulting database is the most comprehensive and accurate of its kind. By generating a score that reflects the strength of the association, it provides an important tool for the rapid and flexible analysis of large datasets from various high-throughput screening experiments. Furthermore, it can be used for selecting subsets of genes for functional studies, for building disease-specific arrays, for looking at genes common to multiple diseases and various other high-throughput applications. In the future, it will be possible to enhance the utility of the MedGene database by building links between genes and other MeSH terms as well as other biological processes and concepts, such as cell division and responses to small molecules.

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Supporting Information Available: Twenty-three human disease category headings along with all of their child terms selected from the 2002 MeSH index (Supplemental Table 1); analysis of the causes of false negatives in MedGene (Supplemental Table 2); meaningful gene-disease relationships found in MedGene (Supplemental Table 3); causes for incorrect assignment of gene indexes (Supplemental Table 4); a review of the results, showing that the resulting disease clusters were indeed logical (Supplemental Figure 1); and a review of the results showing that among the 505 previously unrelated genes, 467 were either newly identified genes or genes that had not previously been associated with any disease (Supplemental Figure 2). This material is available free of charge via the Internet at <http://pubs.acs.org> and at the web sites mentioned in the text.

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Exhibit 1

GNE.3230R1C39

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant	:	Eaton, et al.
Appl. No.	:	10/063,557
Filed	:	May 2, 2002
For	:	SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
Examiner	:	David J. Blanchard
Group Art Unit	:	1642

DECLARATION OF J. CHRISTOPHER GRIMALDI, UNDER 37 CFR §1.132

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Sir:

I, J. Christopher Grimaldi, declare and state as follows:

1. I am a Senior Research Associate in the Molecular Biology Department of Genentech, Inc., South San Francisco, CA 94080.
2. My scientific Curriculum Vitae, including my list of publications, is attached to and forms part of this Declaration (Exhibit A).
3. I joined Genentech in January of 1999. From 1999 to 2003, I directed the Cloning Laboratory in the Molecular Biology Department. During this time I directed or performed numerous molecular biology techniques including semi-quantitative Polymerase Chain Reaction (PCR) analyses. I am currently involved, among other projects, in the isolation of genes coding for membrane associated proteins which can be used as targets for antibody therapeutics against cancer. In connection with the above-identified patent application, I personally performed or directed the semi-quantitative PCR gene expression analyses in the assay entitled "Tumor Versus Normal Differential Tissue Expression Distribution," which is described in EXAMPLE 18 in the specification. These studies were used to identify differences in gene expression between tumor tissue and their normal counterparts.
4. EXAMPLE 18 reports the results of the PCR analyses conducted as part of the investigating of several newly discovered DNA sequences. This process included developing

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primers and analyzing expression of the DNA sequences of interest in normal and tumor tissues. The analyses were designed to determine whether a difference exists between gene expression in normal tissues as compared to tumor in the same tissue type.

5. The DNA libraries used in the gene expression studies were made from pooled samples of normal and of tumor tissues. Data from pooled samples is more likely to be accurate than data obtained from a sample from a single individual. That is, the detection of variations in gene expression is likely to represent a more generally relevant condition when pooled samples from normal tissues are compared with pooled samples from tumors in the same tissue type.

6. In differential gene expression studies, one looks for genes whose expression levels differ significantly under different conditions, for example, in normal versus diseased tissue. Thus, I conducted a semi-quantitative analysis of the expression of the DNA sequences of interest in normal versus tumor tissues. Expression levels were graded according to a scale of +, -, and +/- to indicate the amount of the specific signal detected. Using the widely accepted technique of PCR, it was determined whether the polynucleotides tested were more highly expressed, less expressed, or whether expression remained the same in tumor tissue as compared to its normal counterpart. Because this technique relies on the visual detection of ethidium bromide staining of PCR products on agarose gels, it is reasonable to assume that any detectable differences seen between two samples will represent at least a two fold difference in cDNA.

7. The results of the gene expression studies indicate that the genes of interest can be used to differentiate tumor from normal. The precise levels of gene expression are irrelevant; what matters is that there is a relative difference in expression between normal tissue and tumor tissue. The precise type of tumor is also irrelevant; again, the assay was designed to indicate whether a difference exists between normal tissue and tumor tissue of the same type. If a difference is detected, this indicates that the gene and its corresponding polypeptide and antibodies against the polypeptide are useful for diagnostic purposes, to screen samples to differentiate between normal and tumor. Additional studies can then be conducted if further information is desired.

8. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

By:

J Christopher Grimaldi

Date:

8/10/2004

J. Christopher Grimaldi

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EDUCATION

University of California, Berkeley
Bachelor of Arts in Molecular Biology, 1984

EMPLOYMENT EXPERIENCE

SRA

Genentech Inc., South San Francisco; 1/99 to present

Previously, was responsible to direct and manage the Cloning Lab. Currently focused on isolating cancer specific genes for the Tumor Antigen (TAP), and Secreted Tumor Protein (STOP) projects for the Oncology Department as well as Immunologically relevant genes for the Immunology Department. Directed a lab of 6 scientists focused on a company-wide team effort to identify and isolate secreted proteins for potential therapeutic use (SPDI). For the SPDI project my duties were, among other things, the critically important coordination of the cloning of thousands of putative genes, by developing a smooth process of communication between the Bioinformatics, Cloning, Sequencing, and Legal teams. Collaborated with several groups to discover novel genes through the Curagen project, a unique differential display methodology. Interacted extensively with the Legal team providing essential data needed for filing patents on novel genes discovered through the SPDI, TAP and Curagen projects. My group has developed, implemented and patented high throughput cloning methodologies that have proven to be essential for the isolation of hundreds of novel genes for the SPDI, TAP and Curagen projects as well as dozens of other smaller projects.

Scientist

DNAX Research Institute, Palo Alto; 9/91 to 1/99

Involved in multiple projects aimed at understanding novel genes discovered through bioinformatics studies and functional assays. Developed and patented a method for the specific depletion of eosinophils in vivo using monoclonal antibodies. Developed and implemented essential technical methodologies and provided strategic direction in the areas of expression, cloning, protein purification, general molecular biology, and monoclonal antibody production. Trained and supervised numerous technical staff.

Facilities

Manager

Corixa, Redwood City; 5/89 - 7/91.

Directed plant-related activities, which included expansion planning, maintenance, safety, purchasing, inventory control, shipping and receiving, and laboratory management. Designed and implemented the safety program. Also served as liaison to regulatory agencies at the local, state and federal level. Was in charge of property leases, leasehold improvements, etc. Negotiated vendor contracts and directed the purchasing department. Trained and supervised personnel to carry out the above-mentioned duties.

SRA

University of California, San Francisco
Cancer Research Institute; 2/87-4/89.

Was responsible for numerous cloning projects including: studies of somatic hypermutation, studies of AIDS-associated lymphomas, and cloning of t(5;14), t(11;14), and t(8;14) translocations. Focused on the activation of hemopoietic growth factors involved in the t(5;14) translocation in leukemia patients..

Research
Technician

Berlex Biosciences, South San Francisco; 7/85-2/87.

Worked on a subunit porcine vaccine directed against *Mycoplasma hyopneumoniae*. Was responsible for generating genomic libraries, screening with degenerate oligonucleotides, and characterizing and expressing clones in *E. coli*. Also constructed a general purpose expression vector for use by other scientific teams.

PUBLICATIONS

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MANUSCRIPTS IN PREPARATION

1. Sriram Balasubramanian, J. Christopher Grimaldi, J. Fernando Bazan, Gerard Zurawski and Maureen Howard. "Structural and functional characterization of CD38: Identification of active site residues"

PATENTS

1. "Methods for Eosinophil Depletion with Antibody to CCR3 Receptor" (US 6,207,155 B1).
2. "Amplification Based Cloning Method." (US 6,607,899)
3. Ashkenazi et al., "Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same." (this patent covers several hundred genes)
4. "IL-17 Homologous Polypeptides and Therapeutic Uses Thereof"
5. "Method of Diagnosing and Treating Cartilaginous Disorders."

MEMBERSHIPS AND ACTIVITIES

Editor	Frontiers in Bioscience
Member	DNAX Safety Committee 1991-1999
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Review

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Proteome analysis: Biological assay or data archive?

In this review we examine the current state of proteome analysis. There are three main issues discussed: why it is necessary to study proteomes; how proteomes can be analyzed with current technology; and how proteome analysis can be used to enhance biological research. We conclude that proteome analysis is an essential tool in the understanding of regulated biological systems. Current technology, while still mostly limited to the more abundant proteins, enables the use of proteome analysis both to establish databases of proteins present, and to perform biological assays involving measurement of multiple variables. We believe that the utility of proteome analysis in future biological research will continue to be enhanced by further improvements in analytical technology.

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1 Introduction

A proteome has been defined as the protein complement expressed by the genome of an organism, or, in multicellular organisms, as the protein complement expressed by a tissue or differentiated cell [1]. In the most common implementation of proteome analysis the proteins extracted from the cell or tissue analyzed are separated by high

resolution two-dimensional gel electrophoresis (2-DE), detected in the gel and identified by their amino acid sequence. The ease, sensitivity and speed with which gel-separated proteins can be identified by the use of recently developed mass spectrometric techniques have dramatically increased the interest in proteome technology. One of the most attractive features of such analyses is that complex biological systems can potentially be studied in their entirety, rather than as a multitude of individual components. This makes it far easier to uncover the many complex, and often obscure, relationships between mature gene products in cells. Large-scale proteome characterization projects have been undertaken for a number of different organisms and cell types. Microbial proteome projects currently in progress include, for example: *Saccharomyces cerevisiae* [2], *Salmonella enterica* [3], *Spiroplasma melliferum* [4], *Mycobacterium tuberculosis* [5], *Ochrobactrum anthropi* [6], *Haemophilus influenzae* [7], *Synechocystis* spp. [8], *Escherichia coli* [9], *Rhizobium leguminosarum* [10], and *Dictyostelium discoideum* [11]. Proteome projects underway for tissues of more complex organisms include those for: human bladder squamous cell carcinomas [12], human liver [13], human plasma [13], human keratinocytes [12], human fibroblasts [12], mouse kidney [12], and rat serum [14]. In this manuscript we critically assess the concept of proteome analysis and the technical feasibility of establishing complete proteome maps, and discuss ways in which proteome analysis and biological research intersect.

2 Rationale for proteome analysis

The dramatic growth in both the number of genome projects and the speed with which genome sequences are being determined has generated huge amounts of sequence information, for some species even complete genomic sequences ([15–17]). The description of the state of a biological system by the quantitative measurement of system components has long been a primary objective in molecular biology. With recent technical advances including the development of differential display-PCR [18], cDNA microarray and DNA chip technology [19, 20] and serial analysis of gene expression (SAGE) [21, 22], it is now feasible to establish global and quantitative mRNA expression maps of cells and tissues, in which the sequence of all the genes is known, at a speed and sensitivity which is not matched by current

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Abbreviations: CID, collision-induced dissociation; MS/MS, tandem mass spectrometry; SAGE, serial analysis of gene expression

Keywords: Proteome / Two-dimensional polyacrylamide gel electrophoresis / Tandem mass spectrometry

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protein analysis technology. Given the long-standing paradigm in biology that DNA synthesizes RNA which synthesizes protein, and the ability to rapidly establish global, quantitative mRNA expression maps, the questions which arise are why technically complex proteome projects should be undertaken and what specific types of information could be expected from proteome projects which cannot be obtained from genomic and transcript profiling projects. We see three main reasons for proteome analysis to become an essential component in the comprehensive analysis of biological systems. (i) Protein expression levels are not predictable from the mRNA expression levels, (ii) proteins are dynamically modified and processed in ways which are not necessarily apparent from the gene sequence, and (iii) proteomes are dynamic and reflect the state of a biological system.

2.1 Correlation between mRNA and protein expression levels

Interpretations of quantitative mRNA expression profiles frequently implicitly or explicitly assume that for specific genes the transcript levels are indicative of the levels of protein expression. As part of an ongoing study in our laboratory, we have determined the correlation of expression at the mRNA and protein levels for a population of selected genes in the yeast *Saccharomyces cerevisiae* growing at mid-log phase (S. P. Gygi *et al.*, submitted for publication). mRNA expression levels were calculated from published SAGE frequency tables [22]. Protein expression levels were quantified by metabolic radiolabeling of the yeast proteins, liquid scintillation counting of the protein spots separated by high resolution 2-DE and mass spectrometric identification of the protein(s) migrating to each spot. The selected 80 samples constitute a relatively homogeneous group with respect to predicted half-life and expression level of the protein products. Thus far, we have found a general trend but no strong correlation between protein and transcript levels (Fig. 1). For some genes studied equivalent mRNA transcript levels translated into protein abundances which varied by more than 50-fold. Similarly, equivalent steady-state protein expression levels were maintained by transcript levels varying by as much as 40-fold (S. P. Gygi *et al.*, submitted). These results suggest that even for a population of genes predicted to be relatively homogeneous with respect to protein half-life and gene expression, the protein levels cannot be accurately predicted from the level of the corresponding mRNA transcript.

2.2 Proteins are dynamically modified and processed

In the mature, biologically active form many proteins are post-translationally modified by glycosylation, phosphorylation, prenylation, acylation, ubiquitination or one or more of many other modifications [23] and many proteins are only functional if specifically associated or complexed with other molecules, including DNA, RNA, proteins and organic and inorganic cofactors. Frequently, modifications are dynamic and reversible and may alter the precise three-dimensional structure and the state of activity of a protein. Collectively, the state of modification of the proteins which constitute a biological system

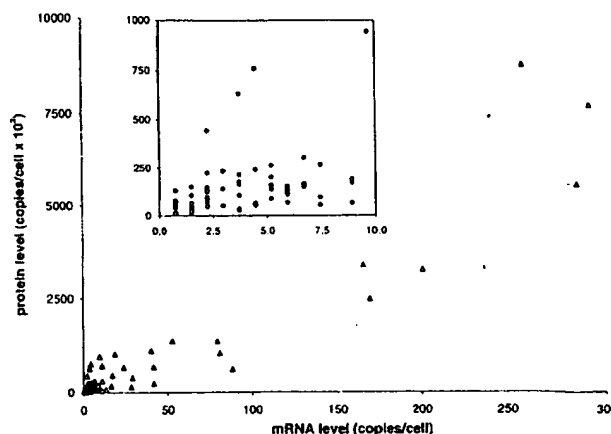


Figure 1. Correlation between mRNA and protein levels in yeast cells. For a selected population of 80 genes, protein levels were measured by ^{35}S -radiolabeling and mRNA levels were calculated from published SAGE tables. Inset: expanded view of the low abundance region. For more experimental details, also see Figs. 5 and 6, (S. P. Gygi *et al.*, submitted).

are important indicators for the state of the system. The type of protein modification and the sites modified at a specific cellular state can usually not be determined from the gene sequence alone.

2.3 Proteomes are dynamic and reflect the state of a biological system

A single genome can give rise to many qualitatively and quantitatively different proteomes. Specific stages of the cell cycle and states of differentiation, responses to growth and nutrient conditions, temperature and stress, and pathological conditions represent cellular states which are characterized by significantly different proteomes. The proteome, in principle, also reflects events that are under translational and post-translational control. It is therefore expected that proteomics will be able to provide the most precise and detailed molecular description of the state of a cell or tissue, provided that the external conditions defining the state are carefully determined. In answer to the question of whether the study of proteomes is necessary for the analysis of biomolecular systems, it is evident that the analysis of mature protein products in cells is essential as there are numerous levels of control of protein synthesis, degradation, processing and modification, which are only apparent by direct protein analysis.

3 Description and assessment of current proteome analysis technology

3.1 Technical requirements of proteome technology

In biological systems the level of expression as well as the states of modification, processing and macro-molecular association of proteins are controlled and modulated depending on the state of the system. Comprehensive analysis of the identity, quantity and state of modification of proteins therefore requires the detection and

quantitation of the proteins which constitute the system, and analysis of differentially processed forms. There are a number of inherent difficulties in protein analysis which complicate these tasks. First, proteins cannot be amplified. It is possible to produce large amounts of a particular protein by over-expression in specific cell systems. However, since many proteins are dynamically post-translationally modified, they cannot be easily amplified in the form in which they finally function in the biological system. It is frequently difficult to purify from the native source sufficient amounts of a protein for analysis. From a technological point of view this translates into the need for high sensitivity analytical techniques. Second, many proteins are modified and processed post-translationally. Therefore, in addition to the protein identity, the structural basis for differentially modified isoforms also needs to be determined. The distribution of a constant amount of protein over several differentially modified isoforms further reduces the amount of each species available for analysis. The complexity and dynamics of post-translational protein editing thus significantly complicates proteome studies. Third, proteins vary dramatically with respect to their solubility in commonly used solvents. There are few, if any, solvent conditions in which all proteins are soluble and which are also compatible with protein analysis. This makes the development of protein purification methods particularly difficult since both protein purification and solubility have to be achieved under the same conditions. Detergents, in particular sodium dodecyl sulfate (SDS), are frequently added to aqueous solvents to maintain protein solubility. The compatibility with SDS is a big advantage of SDS polyacrylamide gel electrophoresis (SDS-PAGE) over other protein separation techniques. Thus, SDS-PAGE and two-dimensional gel electrophoresis, which also uses SDS and other detergents, are the most general and preferred methods for the purification of small amounts of proteins, provided that activity does not necessarily need to be maintained. Lastly, the number of proteins in a given cell system is typically in the thousands. Any attempt to identify and categorize all of these must use methods which are as rapid as possible to allow completion of the project within a reasonable time frame. Therefore, a successful, general proteomics technology requires high sensitivity, high throughput, the ability to differentiate differentially modified proteins, and the ability to quantitatively display and analyze all the proteins present in a sample.

3.2 2-D electrophoresis – mass spectrometry: a common implementation of proteome analysis

The most common currently used implementation of proteome analysis technology is based on the separation of proteins by two-dimensional (IEF/SDS-PAGE) gel electrophoresis and their subsequent identification and analysis by mass spectrometry (MS) or tandem mass spectrometry (MS/MS). In 2-DE, proteins are first separated by isoelectric focusing (IEF) and then by SDS-PAGE, in the second, perpendicular dimension. Separated proteins are visualized at high sensitivity by staining or autoradiography, producing two-dimensional arrays of proteins. 2-DE gels are, at present, the most commonly used means of global display of proteins in complex

samples. The separation of thousands of proteins has been achieved in a single gel [24, 25] and differentially modified proteins are frequently separated. Due to the compatibility of 2-DE with high concentrations of detergents, protein denaturants and other additives promoting protein solubility, the technique is widely used.

The second step of this type of proteome analysis is the identification and analysis of separated proteins. Individual proteins from polyacrylamide gels have traditionally been identified using *N*-terminal sequencing [26, 27], internal peptide sequencing [28, 29], immunoblotting or comigration with known proteins [30]. The recent dramatic growth of large-scale genomic and expressed sequence tag (EST) sequence databases has resulted in a fundamental change in the way proteins are identified by their amino acid sequence. Rather than by the traditional methods described above, protein sequences are now frequently determined by correlating mass spectral or tandem mass spectral data of peptides derived from proteins, with the information contained in sequence databases [31–33].

There are a number of alternative approaches to proteome analysis currently under development. There is considerable interest in developing a proteome analysis strategy which bypasses 2-DE altogether, because it is considered a relatively slow and tedious process, and because of perceived difficulties in extracting proteins from the gel matrix for analysis. However, 2-DE as a starting point for proteome analysis has many advantages compared to other techniques available today. The most significant strengths of the 2-DE-MS approach include the relatively uniform behavior of proteins in gels, the ability to quantify spots and the high resolution and simultaneous display of hundreds to thousands of proteins within a reasonable time frame.

A schematic diagram of a typical procedure of the identification of gel-separated proteins is shown in Fig. 2. Protein spots detected in the gel are enzymatically or chemically fragmented and the peptide fragments are isolated for analysis, as already indicated, most frequently by MS or MS/MS. There are numerous protocols for the generation of peptide fragments from gel-separated proteins. They can be grouped into two categories, digestion in the gel slice [28, 34] or digestion after electrotransfer out of the gel onto a suitable membrane ([29, 35–37] and reviewed in [38]). In most instances either technique is applicable and yields good results. The analysis of MS or MS/MS data is an important step in the whole process because MS instruments can generate an enormous amount of information which cannot easily be managed manually. Recently, a number of groups have developed software systems dedicated to the use of peptide MS and MS/MS spectra for the identification of proteins. Proteins are identified by correlating the information contained in the MS spectra of protein digests or MS/MS spectra of individual peptides with data contained in DNA or protein sequence databases.

The systems we are currently using in our laboratory are based on the separation of the peptides contained in protein digests by narrow bore or capillary liquid chromatog-

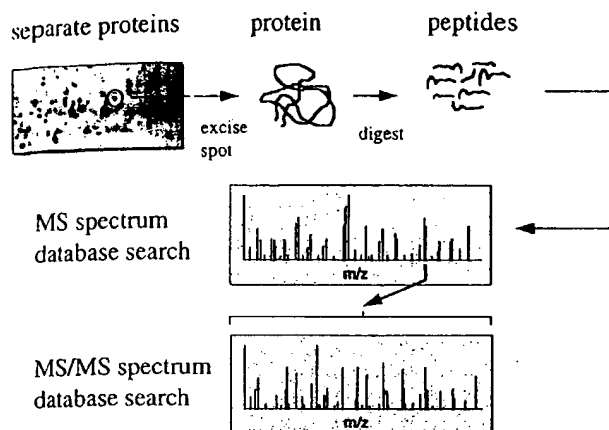


Figure 2. Schematic diagram of a procedure for identification of gel-separated proteins. Peptides can either be separated by a technique such as LC or CE, or infused as a mixture and sorted in the MS. Database searching can either be performed on peptide masses from an MS spectrum, peptide fragment masses from CID spectra of peptides, or a combination of both.

raphy [39, 40] or capillary electrophoresis [41], the analysis of the separated peptides by electrospray ionization (ESI) MS/MS, and the correlation of the generated peptide spectra with sequence databases using the SEQUEST program developed at the University of Washington [32, 33]. The system automatically performs the following operations: a particular peptide ion characterized by its mass-to-charge ratio is selected in the MS out of all the peptide ions present in the system at a particular time; the selected peptide ion is collided in a collision cell with argon (collision-induced dissociation, CID) and the masses of the resulting fragment ions are determined in the second sector of the tandem MS; this experimentally determined CID spectrum is then correlated with the CID spectra predicted from all the peptides in a sequence database which have essentially the same mass as the peptide selected for CID; this correlation matches the isolated peptide with a sequence segment in a database and thus identifies the protein from which the peptide was derived. There are a number of alternative programs which use peptide CID spectra for protein identification, but we use the SEQUEST system because it is currently the most highly automated program and has proven to be successful, versatile and robust.

3.3 Protein identification by LC-MS/MS, capillary LC-MS/MS and CE-MS/MS

It has been demonstrated repeatedly that MS has a very high intrinsic sensitivity. For the routine analysis of gel-separated proteins at high sensitivity, the most significant challenge is the handling of small amounts of sample. The crux of the problem is the extraction and transfer of peptide mixtures generated by the digestion of low nanogram amounts of protein, from gels into the MS/MS system without significant loss of sample or introduction of unwanted contaminants. We employ three different systems for introducing gel-purified samples into an MS, depending on the level of sensitivity

required. As an approximate guideline, for samples containing tens of picomoles of peptides, LC-MS/MS is most appropriate; for samples containing low picomole amounts to high femtomole amounts we use capillary LC-MS/MS; and for samples containing femtomoles or less, CE-MS/MS is the method of choice.

3.3.1 LC-MS/MS

The coupling of an MS to an HPLC system using a 0.5 mm diameter or bigger reverse phase (RP) column has been described in detail [42]. This system has several advantages if a large number of samples are to be analyzed and all are available in sufficient quantity. The LC-MS and database searching program can be run in a fully automated mode using an autosampler, thus maximizing sample throughput and minimizing the need for operator interference. The relatively large column is tolerant of high levels of impurities from either gel preparation or sample matrix. Lastly, if configured with a flow-splitter and micro-sprayer [40], analyses can be performed on a small fraction of the sample (less than 5%) while the remainder of the sample is recovered in very pure solvents. This latter feature is particularly useful when an orthogonal technique is also used to analyze peptide fractions, such as scintillation of an introduced radiolabel, and this data can be correlated with peptides identified by CID spectra.

3.3.2 Capillary LC-MS

An increase of sensitivity of approximately tenfold can be achieved by using a capillary LC system with a 100 μ m ID column rather than a 0.5 mm ID column as referred to above. Since very low flow rates are required for such columns, most reports have used a precolumn flow splitting system for producing solvent gradients. We have recently described the design and construction of a novel gradient mixing system which enables the formation of reproducible gradients at very low flow rates (low nL/min) without the need for flow splitting (A. Ducret *et al.*, submitted for publication). Using this capillary LC-MS/MS system we were able to identify gel-separated proteins if low picomole to high femtomole amounts were loaded onto the gel [40]. This system is as yet not automated and, like all capillary LC systems, is prone to blockage of the columns by microparticulates when analyzing gel-separated proteins.

3.3.3 CE-MS/MS

The highest level of sensitivity for analyzing gel-separated proteins can be achieved by using capillary electrophoresis – mass spectrometry (CE-MS). We have described in the past a solid-phase extraction capillary electrophoresis (SPE-CE) system which was used with triple quadrupole and ion trap ESI-MS/MS systems for the identification of proteins at the low femtomole to sub-femtomole sensitivity level [43, 44]. While this system is highly sensitive, its operation is labor-intensive and its operation has not been automated. In order to devise an analytical system with both the sensitivity of a CE and the level of automation of LC, we have constructed

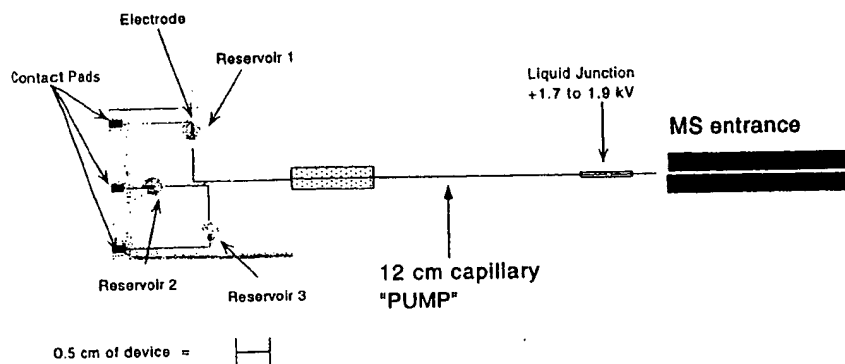


Figure 3. Schematic illustration of a microfabricated analytical system for CE, consisting of a micromachined device, coated capillary electroosmotic pump, and microelectrospray interface. The dimensions of the channels and reservoir are as indicated in the text. The channels on the device were graphically enhanced to make them more visible. Reproduced from [45], with permission.

microfabricated devices for the introduction of samples into ESI-MS for high-sensitivity peptide analysis.

The basic device is a piece of glass into which channels of 10–30 μm in depth and 50–70 μm in diameter are etched by using photolithography/etching techniques similar to the ones used in the semiconductor industry. (A simple device is shown in Fig. 3). The channels are connected to an external high voltage power supply [45]. Samples are manipulated on the device and off the device to the MS by applying different potentials to the reservoirs. This creates a solvent flow by electroosmotic pumping which can be redirected by changing the position of the electrode. Therefore, without the need for valves or gates and without any external pumping, the flow can be redirected by simply switching the position of the electrodes on the device. The direction and rate of the flow can be modulated by the size and the polarity of the electric field applied and also by the charge state of the surface.

The type of data generated by the system is illustrated in Fig. 4, which shows the mass spectrum of a peptide sample representing the tryptic digest of carbonic anhydrase at 290 fmol/ μL . Each numbered peak indicates a peptide successfully identified as being derived from carbonic an-

hydrase. Some of the unassigned signals may be chemical or peptide contaminants. The MS is programmed to automatically select each peak and subject the peptide to CID. The resulting CID spectra are then used to identify the protein by correlation with sequence databases. Therefore, this system allows us to concurrently apply a number of protein digests onto the device, to sequentially mobilize the samples, to automatically generate CID spectra of selected peptide ions and to search sequence databases for protein identification. These steps are performed automatically without the need for user input and proteins can be identified at very low femtomole level sensitivity at a rate of approximately one protein per 15 min.

3.4 Assessment of 2-DE-MS proteome technology

Using a combination of the analytical techniques described above we have identified the 80 protein spots indicated in Fig. 5. The protein pattern was generated by separating a total of 40 microgram of protein contained in a total cell lysate of the yeast strain YPH499 by high resolution 2-DE and silver staining of the separated proteins. To estimate how far this type of proteome analysis can penetrate towards the identification of low abundance proteins, we have calculated the codon bias of the genes encoding the respective proteins. Codon bias is a

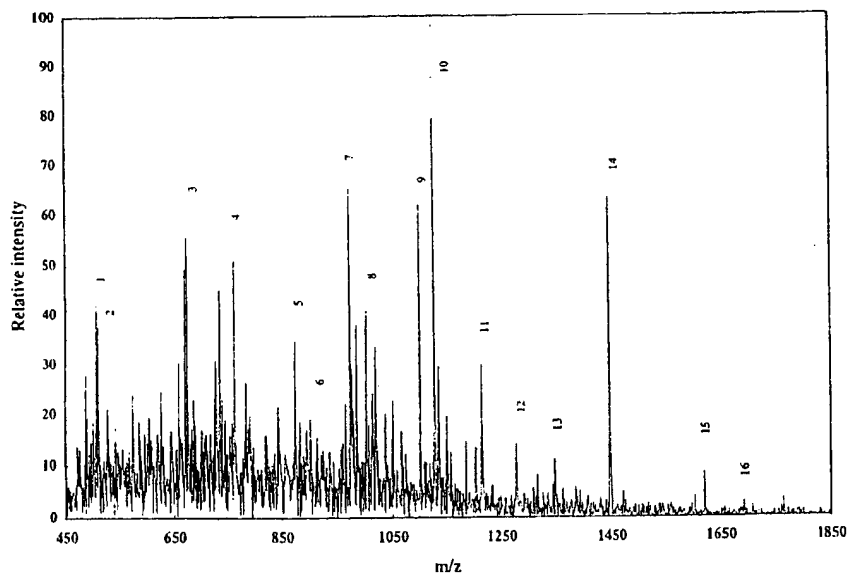


Figure 4. MS spectrum of a tryptic digest of carbonic anhydrase using the microfabricated system shown in Fig. 3. 290 fmol/ μL of carbonic anhydrase tryptic digest was infused into a Finnigan LCQ ion trap MS. Each peak was selected for CID, and those which were identified as containing peptides derived from carbonic anhydrase are numbered. Reproduced from [45], with permission.

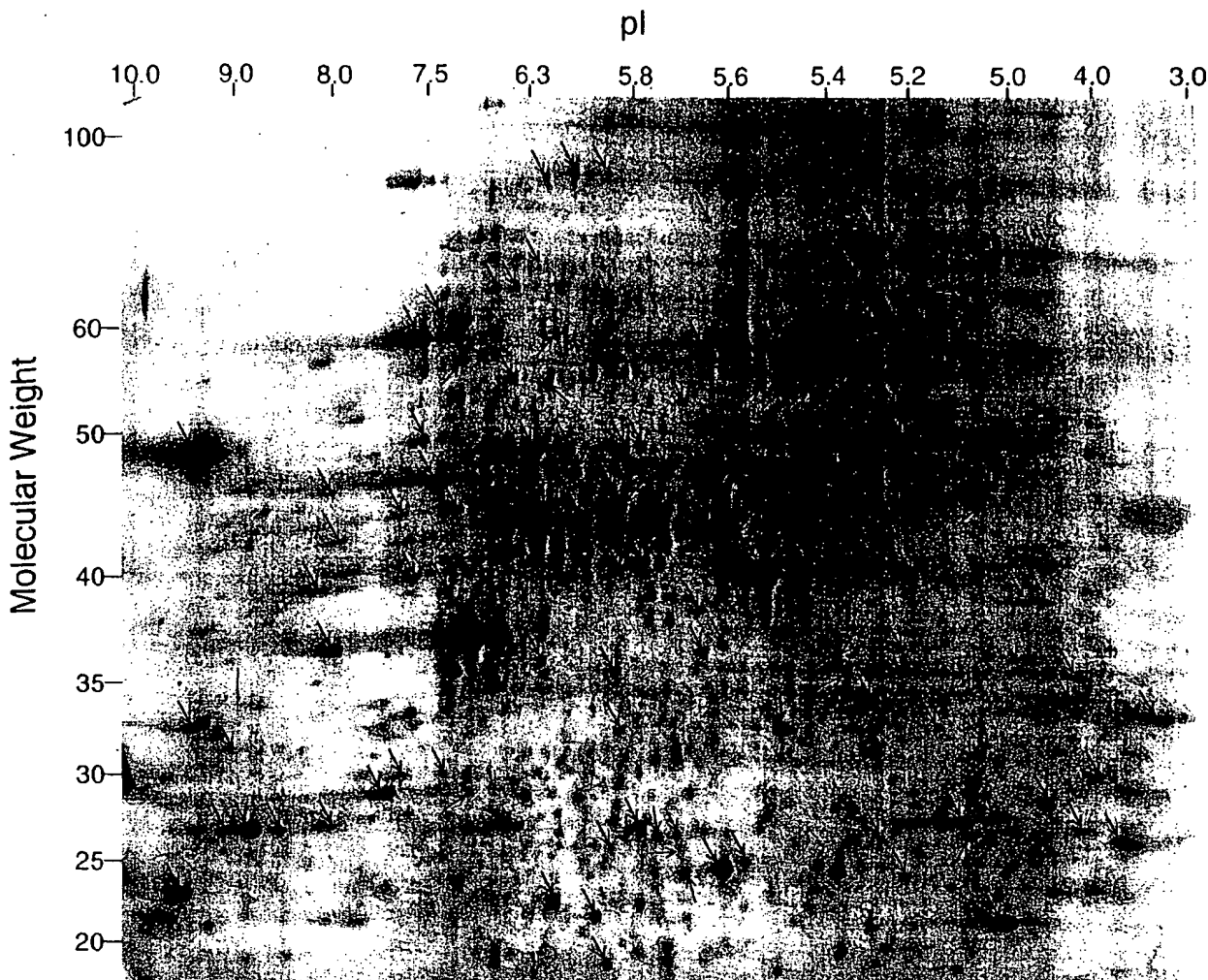


Figure 5. 2-DE separation of a lysate of yeast cells, with identified proteins highlighted. The first dimension of separation was an IPG from pH 3–10, and the second dimension was a 10%T SDS-PAGE gel. Proteins were visualized by silver staining. Further details of experimental procedures are included in S. P. Gygi *et al.* (submitted).

calculated measure of the degree of redundancy of triplet DNA codons used to produce each amino acid in a particular gene sequence. It has been shown to be a useful indicator of the level of the protein product of a particular gene sequence present in a cell [46]. The general rule which applies is that the higher the value of the codon bias calculated for a gene, the more abundant the protein product of that gene becomes. The calculated codon bias values corresponding to the proteins identified in Fig. 5 are shown in Fig. 6b. Nearly all of the proteins identified (> 95%) have codon bias values of > 0.2, indicating they are highly abundant in cells. In contrast, codon bias values calculated for the entire yeast genome (Fig. 6a) show that the majority of proteins present in the proteome have a codon bias of < 0.2 and are thus of low abundance.

This finding is of considerable importance in our assessment of the current status of proteome analysis technology. It is clear that even using highly sensitive analytical techniques, we are only able to visualize and identify the

more abundant proteins. Since many important regulatory proteins are present only at low abundance, these would not be amenable to analysis using such techniques. This situation would be exacerbated in the analysis of proteomes containing many more proteins than the approximately 6000 gene products present in yeast cells [16]. In the analysis of, for example, the proteome of any human cells, there are potentially 50 000–100 000 gene products [47]. Inherent limitations on the amount of protein that can be loaded on 2-DE, and the number of components that can be resolved, indicate that only the most highly abundant fraction of the many gene products could be successfully analyzed. One approach that has been employed to circumvent these limitations is the use of very narrow range immobilized pH gradient strips for the first-dimension separation of 2-DE [48]. Since only those proteins which focus within the narrow range will enter the second dimension of separation, a much higher sample loading within the desired range is possible. This, in turn, can lead to the visualization and identification of less abundant proteins.

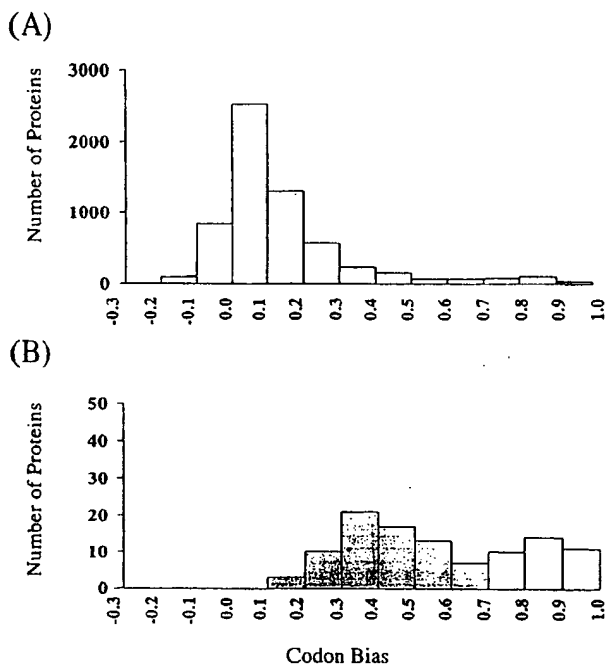


Figure 6. Calculated codon bias values for yeast proteins. (A) Distribution of calculated values for the entire yeast proteome. (B) Distribution of calculated values for the subset of 80 identified proteins also shown in Figs. 1 and 5. Further details of experimental procedures are included in S. P. Gygi *et al.* (submitted).

4 Utility of proteome analysis for biological research

For the success of proteomics as a mainstream approach to the analysis of biological systems it is essential to define how proteome analysis and biological research projects intersect. Without a clear plan for the implementation of proteome-type approaches into biological research projects the full impact of the technology can not be realized. The literature indicates that proteome analysis is used both as a database/data archive, and as a biological assay or biological research tool.

4.1 The proteome as a database

The use of proteomics as a database or data archive essentially entails an attempt to identify all the proteins in a cell or species and to annotate each protein with the known biological information that is relevant for each protein. The level of annotation can, of course, be extensive. The most common implementation of this idea is the separation of proteins by high resolution 2-DE, the identification of each detected protein spot and the annotation of the protein spots in a 2-DE gel database format. This approach is complicated by the fact that it is difficult to precisely define a proteome and to decide which proteome should be represented in the database. In contrast to the genome of a species, which is essentially static, the proteome is highly dynamic. Processes such as differentiation, cell activation and disease can all significantly change the proteome of a species. This is illustrated in Fig. 7. The figure shows two high-resolu-

tion 2-DE maps of proteins isolated from rat serum. Fig. 7A is from the serum of normal rats, while Fig. 7B is from the serum of rats in acute-phase serum after prior treatment with an inflammation-causing agent [49]. It is obvious that the protein patterns are significantly different in several areas, raising the question of exactly which proteome is being described.

Therefore, a comprehensive proteome database of a species or cell type needs to contain all of the parameters which describe the state and the type of the cells from which the proteins were extracted as well as the software tools to search the database with queries which reflect the dynamics of biological systems. A comprehensive proteome database should be capable of quantitatively describing the fate of each protein if specific systems and pathways are activated in the cell. Specifically, the quantity, the degree of modification, the subcellular location and the nature of molecules specifically interacting with a protein as well as the rate of change of these variables should be described. Using these admittedly stringent criteria, there is currently no complete proteome database. A number of such databases are, however, in the process of being constructed. The most advanced among them, in our opinion, are the yeast protein database YPD [50] (accessible at <http://www.ypd.com>) and the human 2D-PAGE databases of the Danish Centre for Human Genome Research [12] (accessible at <http://biobase.dk/cgi-bin/celis>). While neither can be considered complete as not all of the potential gene products are identified, both contain extensive annotation of supplemental information for many of the spots which are positively identified in reference samples.

4.2 The proteome as a biological assay

The use of proteome analysis as a biological assay or research tool represents an alternative approach to integrating biology with proteomics. To investigate the state of a system, samples are subjected to a specific process that allows the quantitative or qualitative measurement of some of the variables which describe the system. In typical biochemical assays one variable (e.g., enzyme activity) of a single component (e.g., a particular enzyme) is measured. Using proteomics as an assay, multiple variables (e.g., expression level, rate of synthesis, phosphorylation state, etc.) are measured concurrently on many (ideally all) of the proteins in a sample. The use of proteomics as an assay is a less far-reaching proposition than the construction of a comprehensive proteome database. It does, however, represent a pragmatic approach which can be adapted to investigate specific systems and pathways, as long as the interpretation of the results takes into account that with current technology not all of the variables which describe the system can be observed (see Section 3.4).

A common implementation of proteome analysis as a biological assay is when a 2-DE protein pattern generated from the analysis of an experimental sample is compared to an array of reference patterns representing different states of the system under investigation. The state of the experimental system at the time the sample was generated is therefore determined by the quantita-

live comparative analysis of hundreds to a few thousand proteins. Comparative analysis of the 2-DE patterns furthermore highlights quantitative and qualitative differences in the protein profiles which correlate with the state of the system. For this type of analysis it is not essential that all the proteins are identified or even visu-

alized, although the results become more informative as more proteins are compared. It is obvious, however, that the possibility to identify any protein deemed characteristic for a particular state dramatically enhances this approach by opening up new avenues for experimentation.

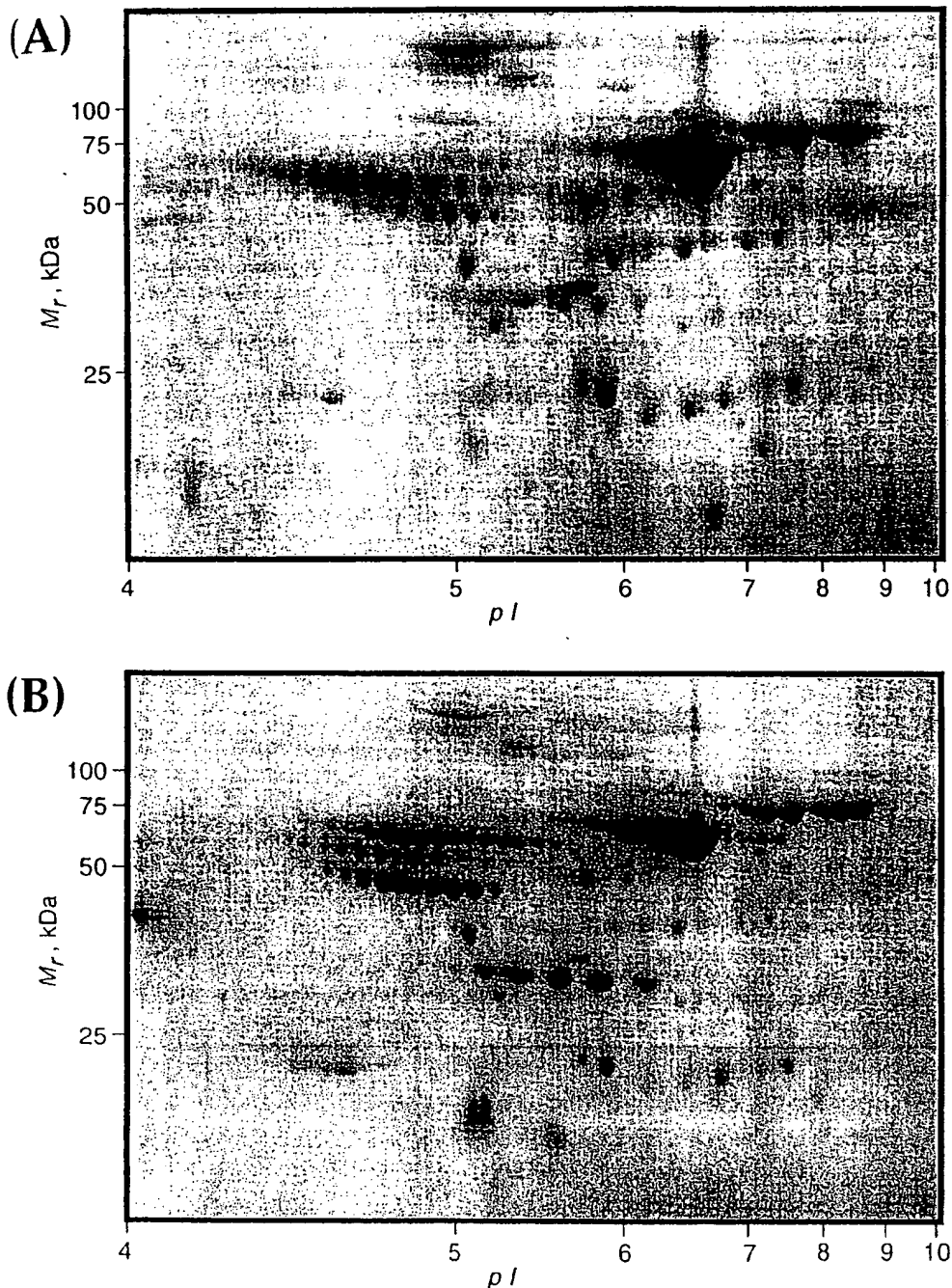


Figure 7. High resolution 2-DE map of proteins isolated from rat serum with or without prior exposure to an inflammation-causing agent. (A) normal rat serum, (B) acute-phase serum from rats which had previously been exposed to an inflammation-causing agent. The first dimension of separation is an IPG from pH 4–10, and the second dimension is a 7.5–17.5%T gradient SDS-PAGE gel. Proteins were visualized by staining with amido black. Further details of experimental procedures are included in [14, 49].

Proteome analysis as a biological assay has been successfully used in the field of toxicology, to characterize disease states or to study differential activation of cells. The approach is limited, of course, by the fact that only the visible protein spots are included in the assay, and it is well known that a substantial but far from complete fraction of cellular proteins are detected if a total cell lysate is separated by 2-DE. Proteins may not be detected in 2-DE gels because they are not abundant enough to be visualized by the detection method used, because they do not migrate within the boundaries (size, *pI*) resolved by the gel, because they are not soluble under the conditions used, or for other reasons.

A different way to use proteome analysis as a biological assay to define the state of a biological system is to take advantage of the wealth of information contained in 2-DE protein patterns. 2-DE is referred to as two-dimensional because of the electrophoretic mobility and the isoelectric points which define the position of each protein in a 2-DE pattern. In addition to the two dimensions used to generate the protein patterns, a number of additional data dimensions are contained in the protein patterns. Some of these dimensions such as protein expression level, phosphorylation state, subcellular location, association with other proteins, rate of synthesis or degradation indicate the activity state of a protein or a biological system. Comparative analysis of 2-DE protein patterns representing different states is therefore ideally suited for the detection, identification and analysis of suitable markers. Once again it must be emphasized that in this type of experiment only a fraction of the cellular proteins is analyzed. Since many regulatory proteins are of low abundance, this limitation is a concern, particularly in cases in which regulatory pathways are being investigated.

5 Concluding remarks

In this report we have addressed three main issues related to proteome analysis. First, we have discussed the rationale for studying proteomes. Second, we have assessed the technical feasibility of analyzing proteomes and described current proteome technology, and third, we have analyzed the utility of proteome analysis for biological research. It is apparent that proteome analysis is an essential tool in the analysis of biological systems. The multi-level control of protein synthesis and degradation in cells means that only the direct analysis of mature protein products can reveal their correct identities, their relevant state of modification and/or association and their amounts. Recently developed methods have enabled the identification of proteins at ever-increasing sensitivity levels and at a high level of automation of the analytical processes. A number of technical challenges, however, remain. While it is currently possible to identify essentially any protein spots that can be visualized by common staining methods, it is apparent that without prior enrichment only a relatively small and highly selected population of long-lived, highly expressed proteins is observed. There are many more proteins in a given cell which are not visualized by such methods. Frequently it is the low abundance proteins that execute key regulatory functions.

We have outlined the two principal ways proteome analysis is currently being used to intersect with biological research projects: the proteome as a database or data archive and proteome analysis as a biological assay. Both approaches have in common that at present they are conceptually and technically limited. Current proteome databases typically are limited to one cell type and one state of a cell and therefore do not account for the dynamics of biological systems. The use of proteome analysis as a biological assay can provide a wealth of information, but it is limited to the proteins detected and is therefore not truly proteome-wide. These limitations in proteomics are to a large extent a reflection of the fact that proteins in their fully processed form cannot easily be amplified and are therefore difficult to isolate in amounts sufficient for analysis or experimentation. The fact that to date no complete proteome has been described further attests to these difficulties. With continued rapid progress in protein analysis technology, however, we anticipate that the goal of complete proteome analysis will eventually become attainable.

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Discordant Protein and mRNA Expression in Lung Adenocarcinomas*

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The relationship between gene expression measured at the mRNA level and the corresponding protein level is not well characterized in human cancer. In this study, we compared mRNA and protein expression for a cohort of genes in the same lung adenocarcinomas. The abundance of 165 protein spots representing 98 individual genes was analyzed in 76 lung adenocarcinomas and nine non-neoplastic lung tissues using two-dimensional polyacrylamide gel electrophoresis. Specific polypeptides were identified using matrix-assisted laser desorption/ionization mass spectrometry. For the same 85 samples, mRNA levels were determined using oligonucleotide microarrays, allowing a comparative analysis of mRNA and protein expression among the 165 protein spots. Twenty-eight of the 165 protein spots (17%) or 21 of 98 genes (21.4%) had a statistically significant correlation between protein and mRNA expression ($r > 0.2445$; $p < 0.05$); however, among all 165 proteins the correlation coefficient values (r) ranged from -0.467 to 0.442 . Correlation coefficient values were not related to protein abundance. Further, no significant correlation between mRNA and protein expression was found ($r = -0.025$) if the average levels of mRNA or protein among all samples were applied across the 165 protein spots (98 genes). The mRNA/protein correlation coefficient also varied among proteins with multiple isoforms, indicating potentially separate isoform-specific mechanisms for the regulation of protein abundance. Among the 21 genes with a significant correlation between mRNA and protein, five genes differed significantly between stage I and stage III lung adenocarcinomas. Using a quantitative analysis of mRNA and protein expression within the same lung adenocarcinomas, we showed that only a subset of the proteins exhibited a significant correlation with mRNA abundance. *Molecular & Cellular Proteomics* 1:304–313, 2002.

Lung cancer is the leading cause of cancer death for both men and women in the United States. Adenocarcinomas of the lung comprise ~40% of all new cases of non-small cell

lung cancer and are now the most common histologic type. Functional genomics, broadly defined as the comprehensive analysis of genes and their products, have become a recent focus of the life sciences (1). Application of these approaches to lung adenocarcinomas has the potential to aid in the identification of high risk patients with resectable early stage lung cancer that may benefit from adjuvant therapy, as well as to identify new therapeutic targets. In human lung cancer, however, little is currently understood regarding the relationship between gene expression as determined by measuring mRNA levels and the corresponding abundance of the protein products.

A number of powerful techniques for analysis of gene expression have been used including differential display (2), serial analysis of gene expression (3), DNA microarrays (4), and proteomics via two-dimensional polyacrylamide gel electrophoresis and mass spectrometry (5). Bioinformatics tools have also been developed to help determine quantitative mRNA/protein expression profiles of all types of cells and tissues (6) and now can be applied to benign and malignant tumors. DNA microarrays (cDNA and oligonucleotide) permit the parallel assessment of thousands of genes and have been utilized in gene expression monitoring (7), polymorphism analysis (8), and DNA sequencing (9). Recent studies have focused on classification or identification of subgroups of lung tumors using DNA microarrays (10, 11). The use of mRNA expression patterns by themselves, however, is insufficient for understanding the expression of protein products, as additional post-transcriptional mechanisms, including protein translation, post-translational modification, and degradation, may influence the level of a protein present in a given cell or tissue. Proteomic analyses, a complementary technology to DNA microarrays for monitoring gene expression, involves protein separation and quantitative assessment of protein spots using 2D¹-PAGE and protein identification using mass spectrometry. By combining proteomic and transcriptional analyses of the same samples, however, it may be possible to understand the complex mechanisms influencing protein expression in human cancer.

In this study, we determined mRNA and protein levels for 165 proteins (98 genes) in 76 lung adenocarcinomas and nine

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¹ The abbreviations used are: 2D, two-dimensional; MALDI-MS, matrix-assisted laser desorption/ionization mass spectrometry.

Protein and mRNA Correlation in Lung Adenocarcinomas

TABLE I

Correlation coefficients of protein and mRNA where only one spot was present on 2D gels

r, correlation coefficient value > 0.2445; p < 0.05. Values in boldface are significant at p < 0.05.

Spot	Unigene	Gene name	r	Protein name
1104	Hs.184510	SFN	0.4337	14-3-3 σ
0894	Hs.77840	ANXA4	0.4219	Annexin IV
1314	Hs.10958	DJ-1	0.3982	DJ-1 protein/MER5
1454	Hs.75428	SOD1	0.3863	Superoxide dismutase (Cu-Zn)
1638	Hs.227751	LGALS1	0.3318	Galectin 1
0264	Hs.129548	HNRPK	0.3034	Transformation up-regulated nuclear protein
1405	Hs.111334	FTL	0.2849	Ferritin light chain
0863	Hs.300711	ANXA5	0.2468	Annexin V
1252	Hs.4745	PSMC	0.2445	26 S proteasome p28
0906	Hs.234489	LDHB	0.4420	L-lactate dehydrogenase H chain (LDH-B)
1171	Hs.241515	COX11	0.2310	COX 11
1160	Hs.181013	PGAM1	0.2023	Phosphoglycerate mutase
0759	Hs.74635	DLD	0.1965	Dihydrolipoamide dehydrogenase precursor
1193	Hs.83383	AOE372	0.1932	Antioxidant enzyme AOE372
0172	Hs.3069	HSPA9B	0.1872	GRP78
0777	Hs.979	PDHB	0.1855	Pyruvate dehydrogenase E1- β subunit precursor
1249	Hs.226795	GSTP1	0.1773	Glutathione S-transferase p1 (GST-p)
1685	Hs.76136	TXN	0.1732	Thioredoxin
1205	Hs.82314	HPRT1	0.1588	HG phosphoribosyltransferase
1230	Hs.279860	TPT1	0.1466	Translationally controlled tumor protein (TCTP)
0803	Hs.181357	LAMR1	0.1463	LAMR
1358	Hs.28914	APRT	0.1399	Adenine phosphoribosyl transferase
1410	Hs.82113	DUT	0.1213	dUTP pyrophosphatase (dUTPase)
1826	Hs.112378	LIMS1	0.1213	Pinch-2 protein
0871	Hs.250502	CA8	0.1122	Carbonic anhydrase-related protein; Syntaxin
0289	Hs.82916	CCT6A	0.1106	Chaperonin-like protein
1143	Hs.11465	GSTTLp28	0.0997	Glutathione S-transferase homolog (GST homolog)
1456	Hs.118638	NME1	0.0932	Nm23 (NDPKA)
1598	Hs.278503	RIG	0.0905	RIG (U32331)
1354	Hs.89761	ATP5D	0.0904	F1F0-type ATP synthase subunit d
1445	Hs.155485	HIP2	0.0843	Huntingtin interacting protein 2 (HIP2)
1479	Hs.177486	APP	0.0748	Amyloid B4A
0608	Hs.182265	KRT19	0.0439	Cytokeratin 19
1071	Hs.10842	RAN	0.0277	GTP-binding nuclear protein RAN(TC4)
0891	Hs.297939	CTSB	0.0264	Cathepsin B
0842	Hs.77274	PLAU	0.0248	Urokinase plasminogen activator
0823	Hs.198248	B4GALT1	0.0183	β 1,4-galactosyl transferase
0613	Hs.1247	APOA4	0.0176	Apolipoprotein A4 (ApoA4)
1338	Hs.104143	CLTA	0.0123	Clathrin light chain A
0902	Hs.5123	SID6-308	0.0117	Cytosolic inorganic pyrophosphatase
1688	Hs.1473	GRP	-0.0040	Preprogastrin-releasing peptide
0265	Hs.274402	HSPA1B	-0.0071	Heat shock-induced protein
1414	Hs.77541	ARF5	-0.0098	ADP-ribosylation factor 1
0710	Hs.97208	HIP1	-0.0114	Huntingtin interacting protein 1 (HIP1)
0632	Hs.170328	MSN	-0.0132	Moesin/E
0525	Hs.284255	ALPP	-0.0148	Alkaline phosphatase, placental
0513	Hs.76901	PDIR	-0.0289	Protein disulfide isomerase-related protein 5
1659	Hs.256897	HINT	-0.0312	Protein kinase C inhibitor
1262	Hs.7016	RAB7	-0.0362	Rab 7 protein
0190	Hs.184411	ALB	-0.0470	Albumin
0948	Hs.2795	LDHA	-0.0549	Lactate dehydrogenase-A (LDHA)
0502	Hs.180532	GPI	-0.0575	Hsp89
0152	Hs.75410	HSPA5	-0.0640	GRP78
1054	Hs.74276	CLIC1	-0.0686	Nuclear chloride channel (RNCC protein)
0709	Hs.253495	SFTPD	-0.0936	Pulmonary surfactant protein D
0887	Hs.78998	PCNA	-0.0982	PCNA
0165	Hs.180414	HSPA8	-0.1014	Heat shock cognate protein, 71 kDa
1109	Hs.75103	YWHAZ	-0.1018	14-3-3 γ/Δ
0197	Hs.554	SSA2	-0.1032	Ro/ss-A antigen

Protein and mRNA Correlation in Lung Adenocarcinomas

TABLE 1—continued

Spot	Unigene	Gene name	r	Protein name
0278	Hs.4112	TCP1	-0.1237	T-complex protein 1, α subunit
1769	Hs.9614	NPM1	-0.1738	B23/nucleolin
0089	Hs.74335	HSPCB	-0.2049	Hsp90
2511	Hs.153179	FABP5	-0.2109	E-FABP/FABP5
1739	Hs.16488	CALR	-0.2344	Calreticulin 32
1138	Hs.301961	GSTM4	-0.2438	Glutathione S-transferase M4 (GST m4)
2533	Hs.77060	PSMB6	-0.2512	Macropain subunit A

non-neoplastic lung tissues. Protein levels were determined using quantitative 2D-PAGE analysis, and the separated protein polypeptides were identified using matrix-assisted laser desorption/ionization mass spectrometry (MALDI-MS). The corresponding mRNA levels for the identified proteins within the same samples were determined using oligonucleotide microarrays. Correlation analyses showed that protein abundance is likely a reflection of the transcription for a subset of proteins, but translation and post-translational modifications also appear to influence the expression levels of many individual proteins in lung adenocarcinomas.

EXPERIMENTAL PROCEDURES

Tissues—Fifty-seven stage I and 19 stage III lung adenocarcinomas, as well as nine non-neoplastic lung tissue samples, were used for protein and mRNA analyses. Patient consent was obtained, and the project was approved by the Institutional Review Board. All tissues were obtained after resection at the University of Michigan Health System between May 1991 and July 1998. Tissues were all snap-frozen in liquid nitrogen and then stored at -80°C . The patients included 46 females and 30 males ranging in age from 40.9 to 84.6 (average 63.8) years. Most patients (66/76) demonstrated a positive smoking history. Sixty-one tumor samples were classified as bronchial-derived, 14 were classified as bronchoalveolar, and one had both features. Eighteen tumor samples were classified as well differentiated, 38 were classified as moderate, and 19 were classified as poorly differentiated adenocarcinomas. Hematoxylin-stained cryostat sections (5 μm), prepared from the same tumor pieces to be utilized for protein and mRNA isolation, were evaluated by a pathologist and compared with hematoxylin- and eosin-stained sections made from paraffin blocks of the same tumors. Specimens were excluded from analysis if they showed unclear or mixed histology (e.g. adenocarcinoma), tumor cellularity less than 70%, potential metastatic origin as indicated by previous tumor history, extensive lymphocytic infiltration, or fibrosis or if the patient had received prior chemotherapy or radiotherapy.

Oligonucleotide Array Hybridization—The HuGeneFL oligonucleotide arrays (Affymetrix, Santa Clara, CA) containing 8800 genes were used in this study. Total RNA was isolated from all samples using Trizol reagent (Invitrogen). The resulting RNA was then subjected to further purification using RNeasy spin columns (Qiagen). Preparation of cRNA, hybridization, and scanning of the HuGeneFL arrays were performed according to the manufacturer's protocol (Affymetrix, Santa Clara, CA). Data analysis was performed using GeneChip 4.0 software. The gene expression profile of each tumor was normalized to the median gene expression profile for the entire sample. Details of data trimming and normalization are described elsewhere (11).

2D-PAGE and Quantitative Protein Analysis—Tissue for both protein and mRNA isolation came from contiguous areas of each sample. Protein separation using 2D-PAGE, silver staining, and digitization

were performed as described previously (12, 13). Our 2D-PAGE system allows us to run 20 gels at one time (one batch). Spot detection and quantification were accomplished utilizing Bio Image Visage System software (Bioimage Corp., Ann Arbor, MI). The integrated intensity of each spot was calculated as the measured optical density units $\times \text{mm}^2$. Of the total possible 2000 spots detectable on each gel, 820 spots on the gel of each sample were matched using a Gel-ed match program with the same spots on a chosen "master" gel. In each sample, 250 ubiquitously expressed reference spots were used to adjust for variations between gels, such as that created by subtle differences in protein loading or gel staining. Slight differences because of batch were corrected after spot-size quantification.

Mass Spectrometry and 2D Western Blotting—Preparative 2D gels were run using extracts from A549 lung adenocarcinoma cells (obtained from ATCC) and using the identical experimental conditions as the analytical 2D gels, except 30% more protein was loaded. The resolved protein gels were silver-stained using successive incubations in 0.02% sodium thiosulfate for 2 min, 0.1% silver nitrate for 40 min, and 0.014% formaldehyde plus 2% sodium carbonate for 10 min. For protein identification, protein polypeptides underwent trypsin digestion followed by MALDI-MS using a MALDI-TOF Voyager-DE mass spectrometer (Perseptive Biosystems, Framingham, MA). The masses were compared with known trypsin digest databases using the MS-FIT database (University of California, San Francisco; prospector.ucsf.edu/ucsfhtml3.2/msfit.htm). Some of the polypeptides included in the analysis had been identified prior to this study on the basis of sequencing (14). The identified protein spots used in this paper are shown in Fig. 1A. The method for 2D-PAGE Western blot verification was as described previously (15). The 2D Western blots of GRP78 and Op18 are shown in Fig. 1, C and E; the others, such as GRP78, GRP75, HSP70, HSC70, KRT8, KRT18, KRT19, Vimentin, ApoJ, 14-3-3, Annexin I, Annexin II, PGP9.5, DJ-1, GST-pl, and PGAM, are described elsewhere.²

Statistical Analysis—Missing values were replaced with the mean value of the protein spot. The transform $x \rightarrow \log(1 + x)$ was applied to normalize all protein expression values. The relationship between protein and mRNA expression levels within the same samples was examined using the Spearman correlation coefficient analysis (16). To identify potentially significant correlations between gene and protein expression, we used an analytical strategy similar to SAM (significance analysis of microarrays) (17), which uses a permutation technique to determine the significance of changes in gene expression between different biological states. To obtain permuted correlation coefficients between gene and protein expression, genes were exchanged first in such a way that permuted correlation coefficient were calculated based on pseudo pairs of genes and proteins. The distribution of permuted correlation coefficients became stable after 60 permutations. This procedure was then repeated 60 times to obtain 60 sets of permuted correlation coefficients. For each of the 60 permutations, the correlations of genes and proteins were ranked

² Chen et al., submitted for publication.

Protein and mRNA Correlation in Lung Adenocarcinomas

TABLE II

Correlation coefficients of protein and mRNA where multiple isoforms were present on 2D gels

r^2 , correlation coefficient value > 0.2445; $p < 0.05$. Values in boldface are significant at $p < 0.05$.

Spot	Unigene	Gene name	r^2	Protein name
1494	Hs.81915	LAP18	0.4003	OP18 (Stathmin)
0957	Hs.77899	TPM1	0.3930	Tropomyosins 1-6
0353	Hs.289101	GRP58	0.3802	Protease disulfide isomerase (GRP58)
0855	Hs.169476	GAPD	0.3693	Glyceraldehyde-3-phosphate dehydrogenase
1198	Hs.41707	HSPB3	0.3668	Hsp27
1203	Hs.83848	TP11	0.3395	Trifose phosphate isomerase (TP11)
0523	Hs.65114	KRT18	0.3335	Cytokeratin 18
1492	Hs.81915	LAP18	0.3234	OP18 (Stathmin)
1493	Hs.81915	LAP18	0.3154	OP18 (Stathmin)
1181	Hs.78225	ANXA1	0.3102	Annexin variant I
0439	Hs.242463	KRT8	0.3049	Cytokeratin 8
0505	Hs.297753	VIM	0.2939	Vimentin
0593	Hs.297753	VIM	0.2809	Vimentin
1874	Hs.75313	AKR1B1	0.2790	Aldose reductase
0935	Hs.75544	YWHAH	0.2775	14-3-3 η
2524	Hs.78225	ANXA1	0.2612	Annexin I
2324	Hs.65114	KRT18	0.2601	Cytokeratin 18
1192	Hs.41707	HSPB3	0.2558	Hsp27
0350	Hs.289101	GRP58	0.2516	Phospholipase C (GRP58)
0992	Hs.75313	AKR1B1	-0.2460	Aldose reductase
0851	Hs.75313	AKR1B1	0.0761	Aldose reductase
0853	Hs.75313	AKR1B1	-0.0675	Aldose reductase
2503	Hs.76392	ALDH1	-0.0565	Aldehyde dehydrogenase
0381	Hs.76392	ALDH1	-0.0371	Aldehyde dehydrogenase
0371	Hs.76392	ALDH1	-0.0680	Aldehyde dehydrogenase
1179	Hs.78225	ANXA1	0.2052	Annexin variant I
0762	Hs.78225	ANXA1	-0.0739	Annexin I
0760	Hs.78225	ANXA1	-0.0228	Annexin I
2506	Hs.217493	ANXA2	0.2223	Lipocotin (annexin II)
0772	Hs.217493	ANXA2	0.2080	Lipocotin (annexin II)
0723	Hs.217493	ANXA2	0.0701	Lipocotin
1239	Hs.93194	APOA1	0.1133	Apolipoprotein A1 (ApoA1)
1237	Hs.93194	APOA1	-0.0373	Apolipoprotein A1 (ApoA1)
1234	Hs.93194	APOA1	-0.0894	Apolipoprotein A1 (ApoA1)
0428	Hs.25	ATP5B	0.0080	ATP synthase β subunit precursor
0427	Hs.25	ATP5B	0.0122	ATP synthase β subunit precursor
0424	Hs.25	ATP5B	-0.0992	ATP synthase β subunit precursor
0883	Hs.75106	CLU	-0.0483	Apolipoprotein J (ApoJ)
0780	Hs.75106	CLU	-0.0443	Apolipoprotein J (ApoJ)
1527	Hs.119140	EIF5A	-0.0726	eIF-5A
1484	Hs.119140	EIF5A	-0.0378	eIF-5A
1728	Hs.5241	FABP1	-0.1916	L-FABP
1712	Hs.5241	FABP1	-0.0473	L-FABP
0947	Hs.169476	GAPD	0.1745	Glyceraldehyde-3-phosphate dehydrogenase
1232	Hs.75207	GLO1	0.2249	Glyoxalase-I
1229	Hs.75207	GLO1	0.0450	Glyoxalase-1
1595	Hs.158300	HAP1	-0.0137	Huntingtin-associated protein 1 (neuroan 1)
1810	Hs.75990	HP	-0.4672	α -Haptoglobin
1459	Hs.75990	HP	0.0802	α -Haptoglobin
1458	Hs.75990	HP	-0.0305	α -Haptoglobin
0619	Hs.75990	HP	0.0461	B-haptoglobin
0615	Hs.75990	HP	-0.0034	B-haptoglobin
1250	Hs.41707	HSPB3	-0.1024	Hsp27
0549	Hs.79037	HSPD1	0.1074	Hsp60
0338	Hs.79037	HSPD1	0.2265	Hsp60
0333	Hs.79037	HSPD1	0.1383	Hsp60
0331	Hs.79037	HSPD1	0.1603	Hsp60
2381	Hs.65114	KRT18	0.2016	Cytokeratin 18
0535	Hs.65114	KRT18	0.1106	Cytokeratin 18

Protein and mRNA Correlation in Lung Adenocarcinomas

TABLE II—continued.
Correlation coefficients of protein and mRNA where multiple isoforms were present on 2D gels

r , correlation coefficient value > 0.2446 ; $p < 0.05$. Values in boldface are significant at $p < 0.05$.

Spot	Unigene	Gene name	r	Protein name
0529	Hs.65114	KRT18	0.1279	Cytokeratin 18
0528	Hs.65114	KRT18	0.0414	Cytokeratin 18
0527	Hs.65114	KRT18	0.0436	Cytokeratin 18
0514	Hs.65114	KRT18	0.0733	Cytokeratin 18
0451	Hs.242463	KRT8	-0.0111	Cytokeratin 8
0446	Hs.242463	KRT8	0.0347	Cytokeratin 8
0444	Hs.242463	KRT8	-0.1311	Cytokeratin 8
0443	Hs.242463	KRT8	0.0942	Cytokeratin 8
1488	Hs.81915	LAP18	0.0495	OP18 (Stathmin)
0321	Hs.75655	P4HB	-0.0546	PDI (proly-4-OH-B)
0320	Hs.75655	P4HB	-0.0041	PDI (proly-4-OH-B)
1063	Hs.75323	PHB	0.0441	Prohibitin
0837	Hs.75323	PHB	0.1402	Prohibitin
0326	Hs.297681	SERPINA1	-0.0227	α -1-Antitrypsin
0322	Hs.297681	SERPINA1	-0.0277	α -1-Antitrypsin
0241	Hs.297681	SERPINA1	-0.0148	α -1-Antitrypsin
1280	Hs.301254	SFTPA1	-0.1488	Pulmonary surfactant-associated protein
1278	Hs.301254	SFTPA1	-0.2040	Pulmonary surfactant-associated protein
0866	Hs.73980	TNNT1	0.1162	Troponin T
0778	Hs.73980	TNNT1	0.0740	Troponin T
1213	Hs.83848	TPH1	0.0024	Triose phosphate isomerase (TPI)
1210	Hs.83848	TPH1	0.0490	Triose phosphate isomerase (TPI)
1207	Hs.83848	TPH1	-0.1615	Triose phosphate isomerase (TPI)
1204	Hs.83848	TPH1	0.0209	Triose phosphate isomerase (TPI)
1202	Hs.83848	TPH1	0.0721	Triose phosphate isomerase (TPI)
1161	Hs.83848	TPH1	0.2265	Triose phosphate isomerase (TPI)
1052	Hs.77899	TPM1	-0.1040	Tropomyosin clean-product
1039	Hs.77899	TPM1	-0.2899	Cytoskeletal tropomyosin
1035	Hs.77899	TPM1	-0.3821	Tropomyosin
0783	Hs.77899	TPM1	0.0757	Tropomyosins 1-5
1574	Hs.194366	TTR	-0.0065	Transthyretin
0809	Hs.194366	TTR	0.0399	Transthyretin multimer
2202	Hs.76118	UCHL1	-0.0220	Ubiquitin carboxyl-terminal hydrolase isozyme L1
1246	Hs.76118	UCHL1	-0.1261	Ubiquitin carboxyl-terminal hydrolase isozyme L1
1242	Hs.76118	UCHL1	0.1473	Ubiquitin carboxyl-terminal hydrolase isozyme L1
0606	Hs.297753	VIM	0.0951	Vimentin
0594	Hs.297753	VIM	-0.2664	Vimentin-derived protein (vid4)
0508	Hs.297753	VIM	0.1008	Vimentin-derived protein (vid2)
0419	Hs.297753	VIM	0.0032	Vimentin-derived protein (vid1)
1279	Hs.75544	YWHAH	0.0059	14-3-3 η

such that $\rho_p(i)$ denotes the i th largest correlation coefficient for p th permutation. Hence, the expected correlation coefficient, $\rho_E(i)$, was the average over the 60 permutations, $\rho_E(i) = \sum_{p=1}^{60} \rho_p(i)/60$. A scatter plot of observed correlations ($\rho(i)$) versus the expected correlations is shown in Fig. 2D. For this study, we chose threshold $\Delta = 0.115$ so that correlation would be considered significant if absolute value of difference between $\rho(i)$ and $\rho_E(i)$ was greater than the threshold. Twenty-nine (including one with observed correlation coefficient -0.4672) of 165 pairs of gene and protein expression were called significant in such criteria, and the permuted data generated an average of 5.1 falsely significant pairs of gene and protein expression. This provided an estimated false discovery rate (the percentage of pairs of gene and protein expression identified by chance) for our data set.

RESULTS

Correlation of Individual Proteins and mRNA Expression within Each Tumor—We have examined quantitatively 165

protein spots on 2D gels representing 98 genes and compared protein levels with mRNA levels for a cohort of 85 lung adenocarcinomas and normal lung samples. Of the 165 protein spots, 69 proteins were represented by only one known spot on 2D gels for an individual gene, whereas 96 protein spots showed multiple protein products from 29 different genes. 2D Western blotting verified the proteins identified by mass spectrometry when specific antibodies were available. Spearman correlation coefficients of the proteins and their associated mRNA for each protein spot were generated using all 76 lung adenocarcinomas and nine non-neoplastic lung tissues (see Tables I and II, and see Figs. 1 and 2). The correlation coefficients (r) ranged from -0.467 to 0.442 (Fig. 2D). A total of 28 protein spots (21 genes) were found to have a statistically significant correlation between expression of

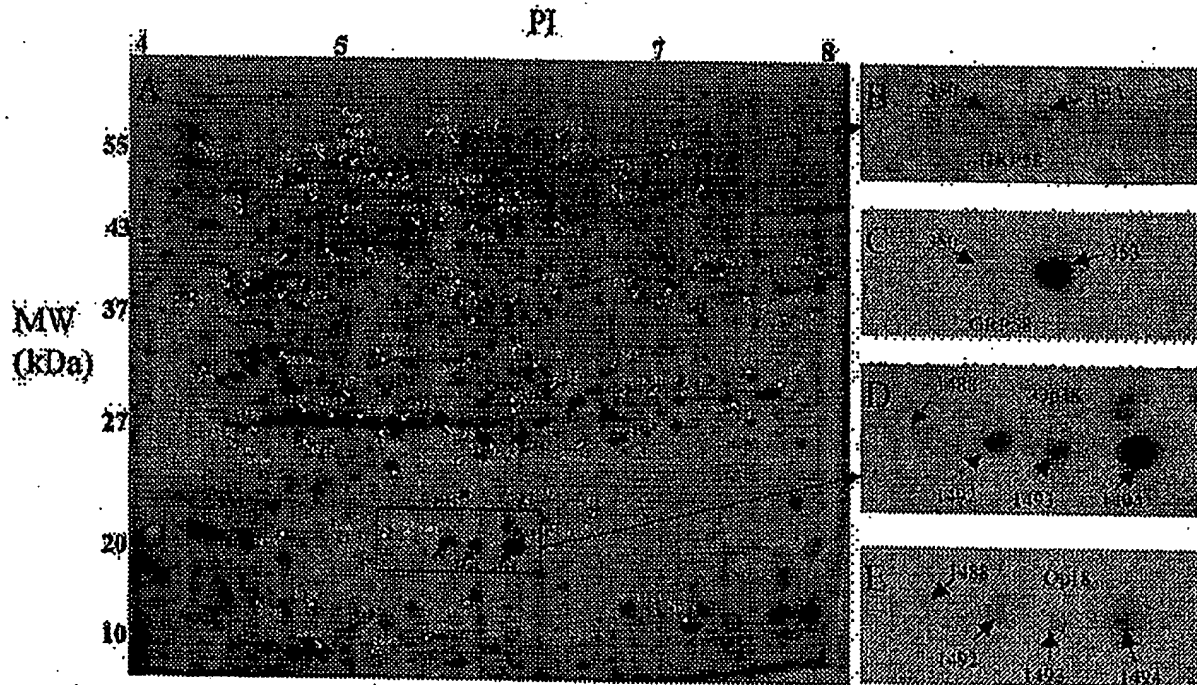


FIG. 1. A, digital image of a silver-stained 2D-PAGE separation of a stage I lung adenocarcinoma showing protein spots separated by molecular mass (MW) and isoelectric point (PI). Twenty-eight protein spots whose expression levels are correlated with mRNA abundance are indicated by the black arrows. B, the outlined areas of A showing protein GRP58. C, 2D Western blot of GRP58 from the A549 lung adenocarcinoma cell line. D, the outlined areas of A showing the protein isoforms of Op18. E, 2D Western blot of Op18 from A549 cells.

their protein and mRNA ($r > 0.2445$; $p < 0.05$). This accounts for 17% (28/165) of the 165 protein spots. Among the 69 genes for which only a single protein spot was known (Table I), nine genes (9/69, 13%) were observed to show a statistically significant relationship between protein and mRNA abundance ($r > 0.2445$; $p < 0.05$). The proteins whose expression levels were correlated with their mRNA abundance included those involved in signal transduction, carbohydrate metabolism, apoptosis, protein post-translational modification, structural proteins, and heat shock proteins (Table III).

Individual Isoforms of the Same Protein Have Different Protein/mRNA Correlation Coefficients.—Of the 165 protein spots, 98 represent protein products of 29 genes with at least two isoforms. Among these 96 protein spots, 19 (19/98 protein spots, 20%) showed a statistically significant correlation between their protein and mRNA expression ($r > 0.2445$; $p < 0.05$) (Table II) and represented 12 genes (12/29, 41%). Individual isoforms of the same protein demonstrated different protein/mRNA correlation coefficients. For example, 2D-PAGE/Western analysis revealed four isoforms of OP18 differing in regards to isoelectric point but similar in molecular weight. Three of the four isoforms (spots 1492, 1493, and 1494) showed a statistically significant correlation between their protein and mRNA abundance ($r = 0.3234$, 0.3154 , and 0.4003 , respectively). The fourth isoform (spot 1488) showed no correlation be-

tween protein and mRNA expression ($r = 0.0495$). Similarly, just one of five quantified isoforms of cytokeratin 8 (spot 439) demonstrated a statistically significant correlation between protein and mRNA abundance ($r = 0.3049$; $p < 0.05$) (Table II).

In addition to differences in the relationship between mRNA levels and protein expression among separate isoforms, some genes with very comparable mRNA levels showed a 24-fold difference in their protein expression. Genes with comparable protein expression levels also showed up to a 28-fold variance in their mRNA levels.

Lack of Correlation for mRNA and Protein Expression when Using Average Tumor Values across All 165 Protein Spots (98 Genes).—The relationship between mRNA and protein expression was also examined by using the average expression values for all samples. To analyze this relationship using this approach, the average value for each protein or mRNA was generated using all 85 lung tissue samples. The range of normalized average protein values ranged from -0.0846 to 0.0979 (raw value 0.0036 to 4.1947), and the range for mRNA was from 0 to 15260.5 for all 165 individual protein spots. The Spearman correlation coefficient for the whole data set (165 protein spots/98 genes) was -0.025 (Fig. 3A). Even for the 28 protein spots (Fig. 2D) that were found to have a statistically significant correlation between their mRNA and protein, use of

Protein and mRNA Correlation in Lung Adenocarcinomas

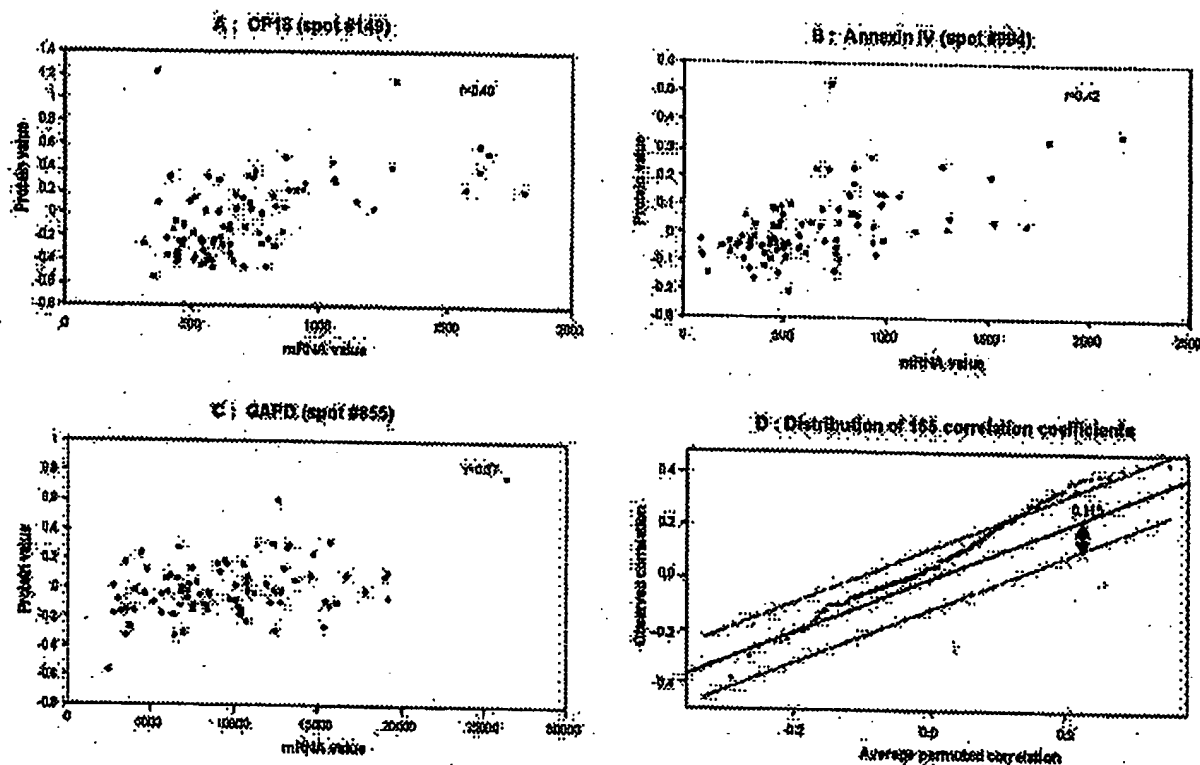


Fig. 2. A–C, plots showing the correlation between mRNA and protein for the three selected genes Op18, Annexin IV, and GAPD for all 76 lung adenocarcinomas and nine non-neoplastic lung samples ($p < 0.05$). D, distribution of all 165 Spearman correlation coefficients (r) and verification analysis using SAM. A more detailed description of the method is provided under "Experimental Procedures." Approximately 17% of the 165 proteins demonstrate a significant correlation between mRNA and protein levels as demonstrated by the values shown beyond the outer range of threshold $\Delta = 0.115$. Normalized protein values were used, thus negative values for some proteins are observed.

the average value resulted in a correlation coefficient value of -0.035 , which was not significant (Fig. 3B).

Lack of a Relationship between Protein/mRNA Correlation Coefficients and Average Protein Abundance—To determine whether an absolute protein level might influence the correlation with mRNA, the mean value of each protein (relative abundance) and the Spearman protein/mRNA correlation coefficients among all 85 samples were examined. No relationship between the protein abundance and the correlation coefficients was observed ($r = 0.039$; $p > 0.05$). A detailed analysis of separate subsets of proteins with differing levels of abundance (less than -0.0014 , larger than -0.0014 , or larger than 0.0077) also showed a lack of correlation between mRNA and protein expression among the 83 (50%), 82 (50%), and 41 (25%) of 165 total protein spots, respectively ($r = 0.016$, 0.08 , and 0.172 , respectively).

Stage-related Changes in the Protein/mRNA Correlation Coefficients—To determine whether the 21 genes (28 protein spots) showing a significant correlation between the protein and mRNA expression among all samples demonstrate changes in this relationship during tumor progression, the correlations were examined separately for stage I ($n = 57$) and

stage III ($n = 19$) lung adenocarcinomas (Table III). The number of non-neoplastic lung samples ($n = 9$) was insufficient for a separate correlation analysis of this group. Many of the protein spots represent one of several known protein isoforms for a given gene. The majority of genes (16/21) did not differ in the protein/mRNA correlation between stage I and stage III tumors indicating a similar regulatory relationship between the mRNA and protein spot. GRP-58, PSMC, SOD1, TPI1, and VIM, however, were found to demonstrate significant differences in the correlation coefficients between stage I and stage III lung adenocarcinomas. For GRP-58, PSMC, and VIM the change in the correlation coefficient was because of a relative increase in protein expression in stage III tumors. For SOD and TPI the change resulted from a relative decrease in expression of this specific protein in stage III tumors.

DISCUSSION

Relatively little is known about the regulatory mechanisms controlling the complex patterns of protein abundance and post-translational modification in tumors. Most reports concerning the regulation of protein translation have focused on

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TABLE III
Stage-dependent analysis of protein-mRNA correlation coefficients

r, correlation coefficient. Values in boldface indicate a significant difference between stage I and stage III.

Spot	Gene name	r (Stage I)	r (Stage III)	Function
1874	AKR1B1	0.269	0.108	Carbohydrate metabolism; electron transporter
2524	ANXA1	0.184	0.572	Phospholipase inhibitor; signal transduction
0994	ANXA4	0.660	0.362	Phospholipase inhibitor
0963	ANXA5	0.241	0.390	Phospholipase inhibitor; calcium binding; phospholipid binding
1314	DJ-1	0.363	0.354	Signal transduction
1405	FTL	0.128	0.358	Iron storage protein
0855	GAPD	0.243	0.581	Carbohydrate metabolism (glycolysis regulation)
0350	GRP58	0.327	-0.087	Signal transduction; protein disulfide isomerase
0284	HNRPK	0.360	0.243	RNA-binding protein (RNA processing/modification)
1192	HSPB3	0.457	0.633	Heat shock protein
0523	KRT18	0.115	0.371	Structural protein
0439	KRT8	0.323	0.438	Structural protein
1492	LAP18	0.483	0.683	Signal transduction; cell growth and maintenance
1638	LGALS1	0.200	0.528	Apoptosis; cell adhesion; cell size control
1252	PSMC	0.253	0.060	Protein degradation
1104	SFN	0.485	0.475	Signal transduction (protein kinase C inhibitor)
1454	SOD1	0.352	0.079	Oxidoreductase
1203	TPH1	0.378	0.009	Carbohydrate metabolism
0957	TPM1	0.475	0.225	Structural protein (muscle); control of heart
0593	VIM	-0.054	0.556	Structural protein
0935	YWHAH	0.283	0.210	Signal transduction

one or several protein products (18). Cells *et al.* (19) found a good correlation between transcript and protein levels among 40 well resolved, abundant proteins using a proteomic and microarray study of bladder cancer. By comparing the mRNA and protein expression levels within the same tumor samples, we found that 17% (28/165) of the protein spots (21/98 genes) show a statistically significant correlation between mRNA and protein. These proteins appear to represent a diverse group of gene products and include those involved in signal transduction, carbohydrate metabolism, protein modification, cell structure, heat shock, and apoptosis. These results suggest that expression of this subset of 165 proteins is likely to be regulated at the transcriptional level in these tissues. The majority of the protein isoforms, however, did not correlate with mRNA levels, and thus their expression is regulated by other mechanisms. We also observed a subset of proteins that demonstrated a negative correlation with the mRNA expression values; for example α -haptoglobin demonstrated a strong negative correlation with its mRNA expression values. This may reflect negative feedback on the mRNA or the protein or the presence of other regulatory influences that are not understood currently.

Post-translational modification or processing will result in individual protein products of the same gene migrating to different locations on 2D-PAGE gels (20). Because the identity of all possible isoforms for each protein examined has not been characterized completely, this may influence the correlation analyses performed in this study. This is partly because of limitations of the 2D-PAGE and mass spectrometry technologies (21, 22). Potential inconsistencies between mRNA and protein correlations that have been reported may also be because of differences, even in the same gene, in the mechanisms of protein translation among different cells or as

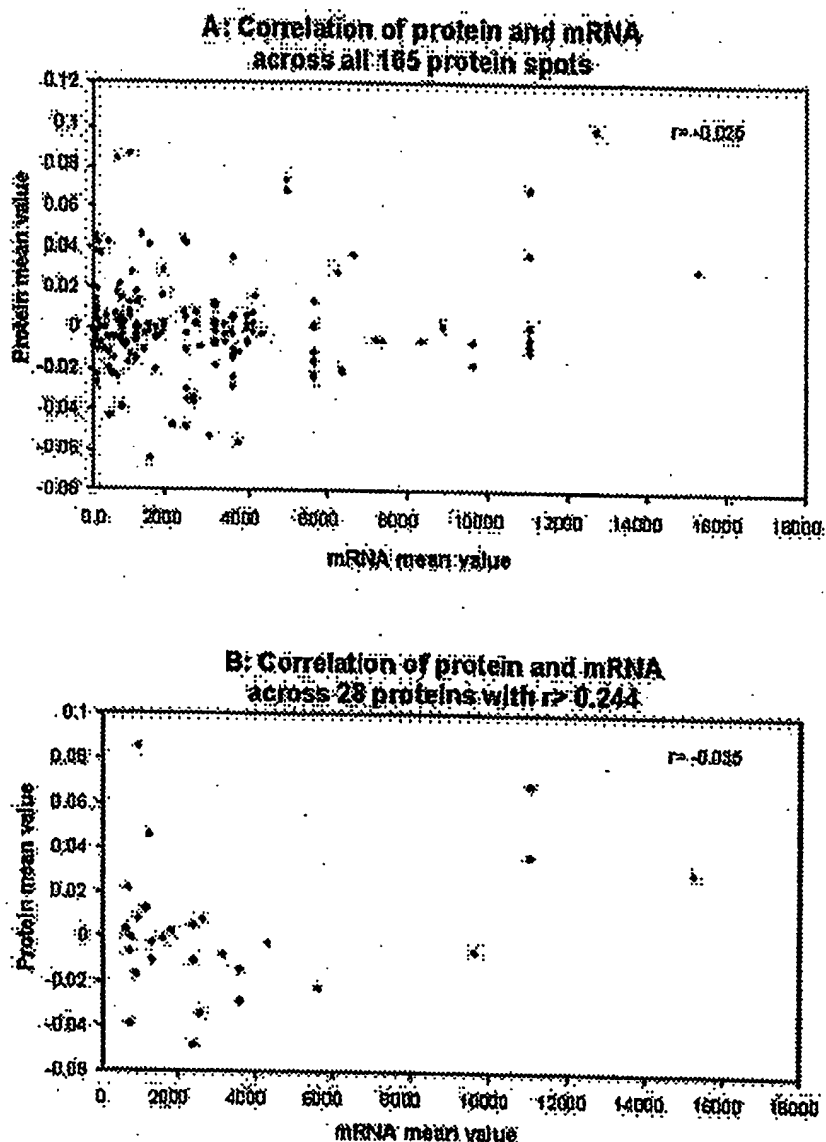
measured in different laboratories (23).

In this study, we examined 165 protein spots identified in lung adenocarcinomas. Ninety-six protein spots, representing the products of 29 genes, contained at least two protein isoforms. Nineteen of 96 protein spots, representing 12 genes, were shown to have a statistically significant correlation between their protein and mRNA expression, suggesting that the levels of these proteins reflects the transcription of the corresponding genes. Differences in protein/mRNA correlations were found among the individual isoforms of a given protein. For example, of the four OP18 isoforms, three showed a statistically significant correlation between the protein and mRNA expression levels. The lack of relationship for the one isoform, however, indicates that individual protein isoforms of the same gene product can be regulated differentially. This is not unexpected and likely reflects other post-translational mechanisms that can influence isoform abundance in tissues and cancer.

In addition to the analyses of the correlation of mRNA/protein within the same tumor samples, we also tested the global relationship between mRNA and the corresponding protein abundance across all 165 protein spots in the lung samples. A protein and mRNA average value for each gene was generated using all 85 lung tissues samples. We observed a very wide range of normalized average protein and mRNA values. The correlation coefficient generated using this average value data set was -0.025, and even for the 28 protein spots that showed a statistically significant correlation between individual mRNA and proteins, the correlation value was only -0.035. This suggests that it is not possible to predict overall protein expression levels based on average

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Fig. 3. The overall correlation of mRNA and protein levels across all 165 protein spots (A) and across 28 protein spots that contained individual r values larger than 0.244 (B) are shown. Each protein or mRNA mean value was calculated based on all 76 lung adenocarcinomas and nine non-neoplastic lung samples using quantitative 2D-PAGE and Affymetrix oligonucleotide microarrays. The Spearman correlation coefficients for the two data sets (A and B) were -0.025 and -0.035 , respectively, indicating a lack of correlation if mean values for mRNA and protein for all samples is used.



mRNA abundance in lung cancer samples. This conclusion is also supported by previous results from Anderson and Sellhammer (24), who examined 19 genes in human liver cells, and by Gygi et al. (25), who examined 106 genes in yeast. Both studies found a lack of correlation between mRNA and protein expression when average or overall levels were used.

A good correlation was reported when the 11 most abundant proteins were examined in yeast (25), suggesting that the level of protein abundance may be a factor that may influence the correlation between mRNA and protein. In the present study, a fairly wide range of mean protein values among 165 protein spots in lung adenocarcinomas was observed, and the correlation coefficients also varied from -0.467 to 0.442 .

A comparison between the mean value of each protein and the correlation coefficient generated using all 85 tissue samples did not reveal a strong relationship between the overall protein abundance and the correlation coefficients ($r = 0.039$; $p > 0.05$). Detailed analysis of different subsets of protein abundance also failed to show a correlation between mRNA and protein expression. Thus in contrast to yeast, a relationship between mRNA/protein correlation coefficient and protein abundance in human lung adenocarcinomas was not observed.

The results of this study indicate that the level of protein abundance in lung adenocarcinomas is associated with the corresponding levels of mRNA in 17% (28 proteins) of the total 165 protein spots examined. This was substantially

higher than the amount predicted to result by chance alone (which was 5.1) and suggests that a transcriptional mechanism likely underlies the abundance of these proteins in lung adenocarcinomas. We also demonstrate that the expression of individual isoforms of the same protein may or may not correlate with the mRNA, indicating that separate and likely post-translational mechanisms account for the regulation of isoform abundance. These mechanisms may also account for the differences in the correlation coefficients observed between stage I and stage III tumors, indicating that specific protein isoforms show regulatory changes during tumor progression. Further studies in lung adenocarcinomas will examine the relationship between the expression of individual protein isoforms and specific clinical-pathological features of these tumors, such as the presence of angiolymphatic invasion, and nodal or pleural surface involvement. The potential to identify specific protein isoforms associated with biological behavior in lung adenocarcinomas would be of considerable interest and will add to our understanding of the regulation of gene products by transcriptional, translational, and post-translational mechanisms.

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Correlation between Protein and mRNA Abundance in Yeast

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We have determined the relationship between mRNA and protein expression levels for selected genes expressed in the yeast *Saccharomyces cerevisiae* growing at mid-log phase. The proteins contained in total yeast cell lysate were separated by high-resolution two-dimensional (2D) gel electrophoresis. Over 150 protein spots were excised and identified by capillary liquid chromatography-tandem mass spectrometry (LC-MS/MS). Protein spots were quantified by metabolic labeling and scintillation counting. Corresponding mRNA levels were calculated from serial analysis of gene expression (SAGE) frequency tables (V. E. Velculescu, L. Zhang, W. Zhou, J. Vogelstein, M. A. Basrai, D. E. Bassett, Jr., P. Hieter, B. Vogelstein, and K. W. Kinzler, *Cell* 88:243-251, 1997). We found that the correlation between mRNA and protein levels was insufficient to predict protein expression levels from quantitative mRNA data. Indeed, for some genes, while the mRNA levels were of the same value the protein levels varied by more than 20-fold. Conversely, invariant steady-state levels of certain proteins were observed with respective mRNA transcript levels that varied by as much as 30-fold. Another interesting observation is that codon bias is not a predictor of either protein or mRNA levels. Our results clearly delineate the technical boundaries of current approaches for quantitative analysis of protein expression and reveal that simple deduction from mRNA transcript analysis is insufficient.

The description of the state of a biological system by the quantitative measurement of the system constituents is an essential but largely unexplored area of biology. With recent technical advances including the development of differential display-PCR (21), of cDNA microarray and DNA chip technology (20, 27), and of serial analysis of gene expression (SAGE) (34, 35), it is now feasible to establish global and quantitative mRNA expression profiles of cells and tissues in species for which the sequence of all the genes is known. However, there is emerging evidence which suggests that mRNA expression patterns are necessary but are by themselves insufficient for the quantitative description of biological systems. This evidence includes discoveries of posttranscriptional mechanisms controlling the protein translation rate (15), the half-lives of specific proteins or mRNAs (33), and the intracellular location and molecular association of the protein products of expressed genes (32).

Proteome analysis, defined as the analysis of the protein complement expressed by a genome (26), has been suggested as an approach to the quantitative description of the state of a biological system by the quantitative analysis of protein expression profiles (36). Proteome analysis is conceptually attractive because of its potential to determine properties of biological systems that are not apparent by DNA or mRNA sequence analysis alone. Such properties include the quantity of protein expression, the subcellular location, the state of modification, and the association with ligands, as well as the rate of change with time of such properties. In contrast to the genomes of a number of microorganisms (for a review, see reference 11) and the transcriptome of *Saccharomyces cerevisiae* (35), which have been entirely determined, no proteome map has been completed to date.

The most common implementation of proteome analysis is the combination of two-dimensional gel electrophoresis (2DE)

(isoelectric focusing-sodium dodecyl sulfate [SDS]-polyacrylamide gel electrophoresis) for the separation and quantitation of proteins with analytical methods for their identification. 2DE permits the separation, visualization, and quantitation of thousands of proteins reproducibly on a single gel (18, 24). By itself, 2DE is strictly a descriptive technique. The combination of 2DE with protein analytical techniques has added the possibility of establishing the identities of separated proteins (1, 2) and thus, in combination with quantitative mRNA analysis, of correlating quantitative protein and mRNA expression measurements of selected genes.

The recent introduction of mass spectrometric protein analysis techniques has dramatically enhanced the throughput and sensitivity of protein identification to a level which now permits the large-scale analysis of proteins separated by 2DE. The techniques have reached a level of sensitivity that permits the identification of essentially any protein that is detectable in the gels by conventional protein staining (9, 29). Current protein analytical technology is based on the mass spectrometric generation of peptide fragment patterns that are idiosyncratic for the sequence of a protein. Protein identity is established by correlating such fragment patterns with sequence databases (10, 22, 37). Sophisticated computer software (8) has automated the entire process such that proteins are routinely identified with no human interpretation of peptide fragment patterns.

In this study, we have analyzed the mRNA and protein levels of a group of genes expressed in exponentially growing cells of the yeast *S. cerevisiae*. Protein expression levels were quantified by metabolic labeling of the yeast proteins to a steady state, followed by 2DE and liquid scintillation counting of the selected, separated protein species. Separated proteins were identified by in-gel tryptic digestion of spots with subsequent analysis by microspray liquid chromatography-tandem mass spectrometry (LC-MS/MS) and sequence database searching. The corresponding mRNA transcript levels were calculated from SAGE frequency tables (35).

This study, for the first time, explores a quantitative comparison of mRNA transcript and protein expression levels for a relatively large number of genes expressed in the same metabolic state. The resultant correlation is insufficient for predic-

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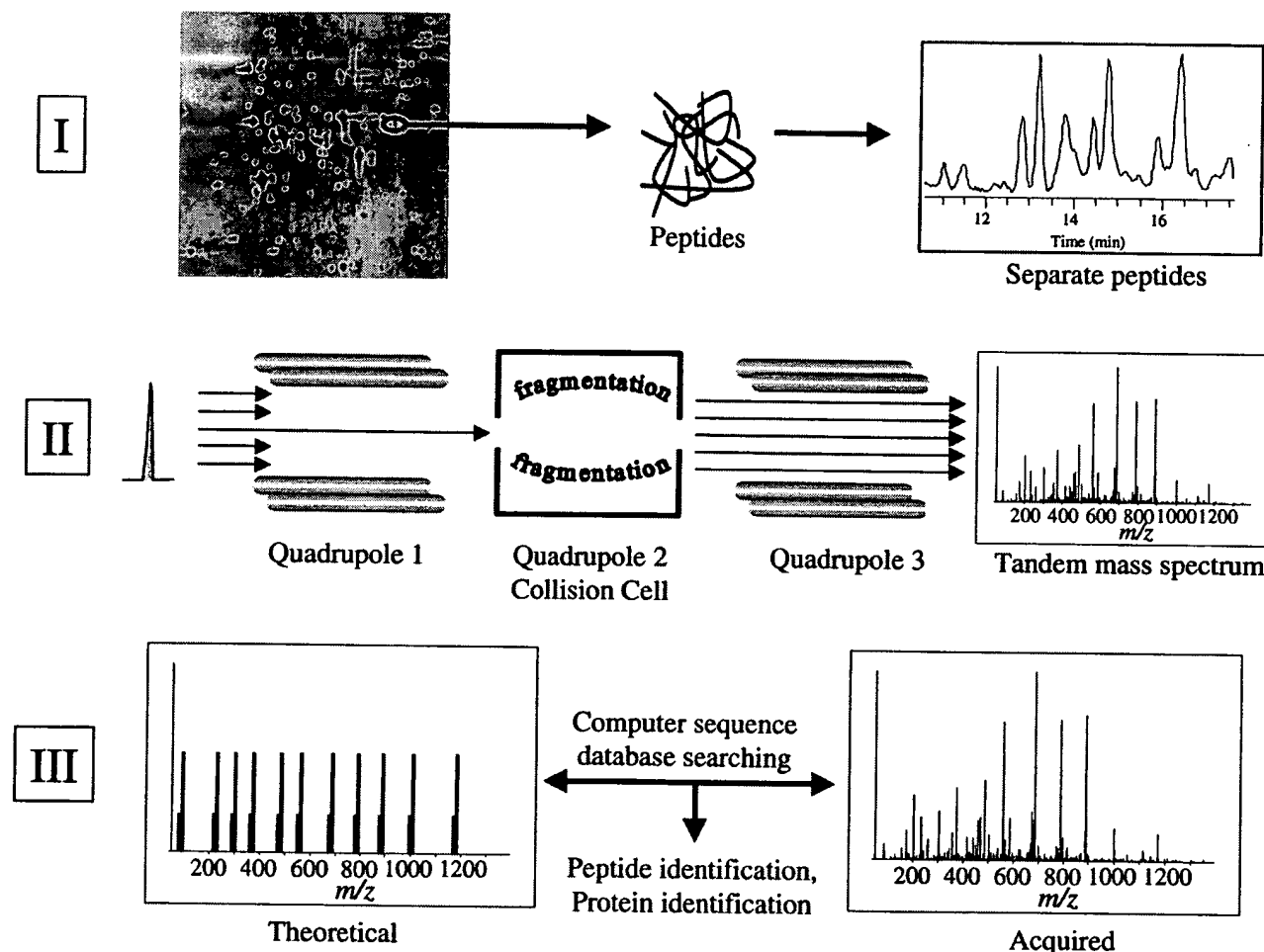


FIG. 1. Schematic illustration of proteome analysis by 2DE and mass spectrometry. In part I, proteins are separated by 2DE, stained spots are excised and subjected to in-gel digestion with trypsin, and the resulting peptides are separated by on-line capillary high-performance liquid chromatography. In part II, a peptide is shown eluting from the column in part I. The peptide is ionized by electrospray ionization and enters the mass spectrometer. The mass of the ionized peptide is detected, and the first quadrupole mass filter allows only the specific mass-to-charge ratio of the selected peptide ion to pass into the collision cell. In the collision cell, the energized, ionized peptides collide with neutral argon gas molecules. Fragmentation of the peptide is essentially random but occurs mainly at the peptide bonds, resulting in smaller peptides of differing lengths (masses). These peptide fragments are detected as a tandem mass (MS/MS) spectrum in the third quadrupole mass filter where two ion series are recorded simultaneously, one each from sequencing inward from the N and C termini of the peptide, respectively. In part III, the MS/MS spectrum from the selected, ionized peptide is compared to predicted tandem mass spectra computer generated from a sequence database. Provided that the peptide sequence exists in the database, the peptide and, by association, the protein from which the peptide was derived can be identified. Unambiguous protein identification is attained in a single analysis because multiple peptides are identified as being derived from the same protein.

tion of protein levels from mRNA transcript levels. We have also compared the relative amounts of protein and mRNA with the respective codon bias values for the corresponding genes. This comparison indicates that codon bias by itself is insufficient to accurately predict either the mRNA or the protein expression levels of a gene. In addition, the results demonstrate that only highly expressed proteins are detectable by 2DE separation of total cell lysates and that therefore the construction of complete proteome maps with current technology will be very challenging, irrespective of the type of organism.

MATERIALS AND METHODS

Yeast strain and growth conditions. The source of protein and message transcripts for all experiments was YPH499 (*MATa ura3-52 lys2-801 ade2-101 leu2-Δ1 his3-Δ200 trp1-Δ63*) (30). Logarithmically growing cells were obtained by growing yeast cells to early log phase (3×10^6 cells/ml) in YPD rich medium (YPD supplemented with 6 mM uracil, 4.8 mM adenine, and 24 mM tryptophan) at 30°C (35). Metabolic labeling of protein was accomplished in YPD medium

exactly as described elsewhere (4) with the exception that 1 ml of cells was labeled with 3 mCi to offset methionine present in YPD medium. Protein was harvested as described by Garrels and coworkers (12). Harvested protein was lyophilized, resuspended in isoelectric focusing gel rehydration solution, and stored at -80°C.

2DE. Soluble proteins were run in the first dimension by using a commercial flatbed electrophoresis system (Multiphor II; Pharmacia Biotech). Immobilized polyacrylamide gel (IPG) dry strips with nonlinear pH 3.0 to 10.0 gradients (Amersham-Pharmacia Biotech) were used for the first-dimension separation. Forty micrograms of protein from whole-cell lysates was mixed with IPG strip rehydration buffer (8 M urea, 2% Nonidet P-40, 10 mM dithiothreitol), and 250 to 380 μ l of solution was added to individual lanes of an IPG strip rehydration tray (Amersham-Pharmacia Biotech). The strips were allowed to rehydrate at room temperature for 1 h. The samples were run at 300 V-10 mA-5 W for 2 h, then ramped to 3,500 V-10 mA-5 W over a period of 3 h, and then kept at 3,500 V-10 mA-5 W for 15 to 19 h. At the end of the first-dimension run (60 to 70 kV·h), the IPG strips were reequilibrated for 8 min in 2% (wt/vol) dithiothreitol in 2% (wt/vol) SDS-6 M urea-30% (wt/vol) glycerol-0.05 M Tris HCl (pH 6.8) and for 4 min in 2.5% iodoacetamide in 2% (wt/vol) SDS-6 M urea-30% (wt/vol) glycerol-0.05 M Tris HCl (pH 6.8). Following reequilibration, the strips were transferred and apposed to 10% polyacrylamide second-dimension gels. Polyacrylamide gels were poured in a casting stand with 10% acrylamide-2.67% piperazine diacrylamide-0.375 M Tris base-HCl (pH 8.8)-0.1% (wt/vol) SDS-0.05%

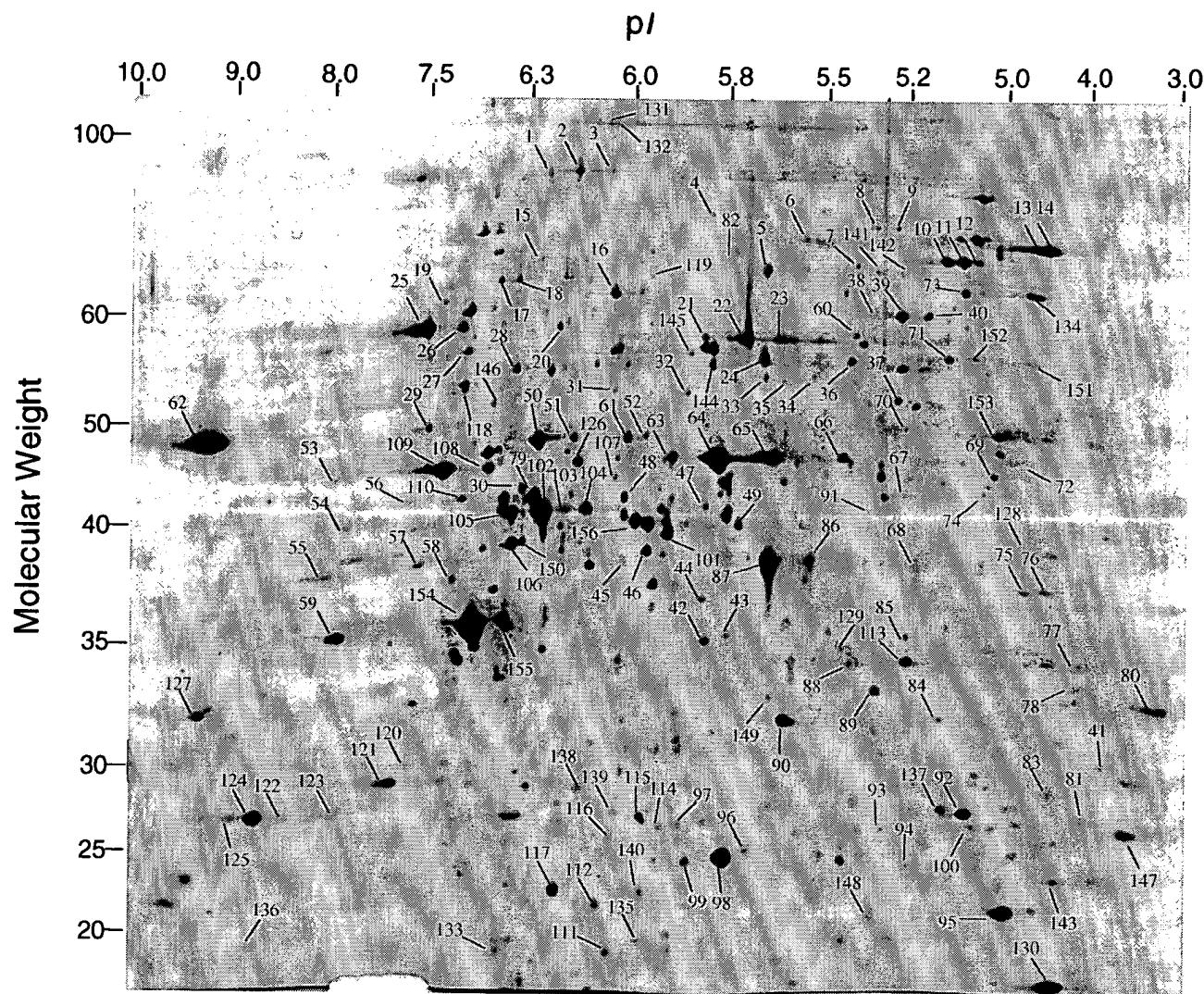


FIG. 2. 2D silver-stained gel of the proteins in yeast total cell lysate. Proteins were separated in the first dimension (horizontal) by isoelectric focusing and then in the second dimension (vertical) by molecular weight sieving. Protein spots (156) were chosen to include the entire range of molecular weights, isoelectric focusing points, and staining intensities. Spots were excised, and the corresponding protein was identified by mass spectrometry and database searching. The spots are labeled on the gel and correspond to the data presented in Table 1. Molecular weights are given in thousands.

(wt/vol) ammonium persulfate–0.05% TEMED (*N,N,N',N'*-tetramethylethylenediamine) in Milli-Q water. The apparatus used to run second-dimension gels was a noncommercial apparatus from Oxford Glycosciences, Inc. Once the IPG strips were apposed to the second-dimension gels, they were immediately run at 50 mA (constant)–500 V–85 W for 20 min, followed by 200 mA (constant)–500 V–85 W until the buffer front line was 10 to 15 mm from the bottom of the gel. Gels were removed and silver stained according to the procedure of Shevchenko et al. (29).

Protein identification. Gels were exposed to X-ray film overnight, and then the silver staining and film were used to excise 156 spots of varying intensities, molecular weights, and isoelectric focusing points. In order to increase the detection limit by mass spectrometry, spots were cut out and pooled from up to four identical cold, silver-stained gels. In-gel tryptic digests of pooled spots were performed as described previously (29). Tryptic peptides were analyzed by microcapillary LC-MS with automated switching to MS/MS mode for peptide fragmentation. Spectra were searched against the composite OWL protein sequence database (version 30.2; 250,514 protein sequences) (24a) by using the computer program Sequest (8), which matches theoretical and acquired tandem mass spectra. A protein match was determined by comparing the number of peptides identified and their respective cross-correlation scores. All protein identifications were verified by comparison with theoretical molecular weights and isoelectric points.

mRNA quantitation. Velculescu and coworkers have previously generated frequency tables for yeast mRNA transcripts from the same strain grown under the same stated conditions as described herein (35). The SAGE technology is based on two main principles. First, a short sequence tag (15 bp) that contains sufficient information uniquely to identify a transcript is generated. A single tag is usually generated from each mRNA transcript in the cell which corresponds to 15 bp at the 3'-most cutting site for *Nla*III. Second, many transcript tags can be concatenated into a single molecule and then sequenced, revealing the identity of multiple tags simultaneously. Over 20,000 transcripts were sequenced from yeast strain YPH499 growing at mid-log phase on glucose. Assuming the previously derived estimate of 15,000 mRNA molecules per cell (16), this would represent a 1.3-fold coverage even for mRNA molecules present at a single copy per cell and would provide a 72% probability of detecting such transcripts. Computer software which took for input the gene detected, examined the nucleotide sequence, and performed the calculation as described by Velculescu and coworkers (35) was written. In practice, we found that for 21 of 128 (16%) genes examined viable mRNA levels from SAGE data could not be calculated. This was because (i) no CATG site was found in the open reading frame (ORF), (ii) a CATG site was found but the corresponding 10-bp putative SAGE tag was not found in the frequency tables, or (iii) identical putative SAGE tags were present for multiple genes (e.g., *TDH2_YEAST* and *TDH3_YEAST*).

TABLE 1. Expressed genes identified from 2D gel in Fig. 2

Mol wt	pI	Spot no.	YPD gene name ^a	Protein abundance (10 ³ copies/cell)	mRNA abundance (copies/cell)	Codon bias
17,259	6.75	133	CPR1	15.2	61.7	0.769
18,702	4.80	83	EGD2	20.1	5.2	0.724
18,726	4.44	147	YKL056C	61.2	88.4	0.831
18,978	5.95	135	YER067W	3.7	6.7	0.118
19,108	5.04	130	YLR109W	94.4	9.7	0.680
19,681	9.08	136	ATP7	11.0	NA ^{b,c}	0.246
20,505	6.07	111	GUK1	16.5	3.7	0.422
21,444	5.25	148	SAR1	5.4	10.4	0.455
21,583	4.98	95	TSA1	110.6	40.1	0.845
22,602	4.30	80	EFB1	66.1	23.8	0.875
23,079	6.29	112	SOD2	12.6	2.2	0.351
23,743	5.44	137	HSP26	NA ^d	0.7	0.434
24,033	5.97	96	ADK1	17.4	16.4	0.656
24,058	4.43	143	YKL117W	29.2	10.4	0.339
24,353	6.30	140	TFS1	8.1	0.7	0.146
24,662	5.85	99	URA5	25.4	6.0	0.359
24,808	6.33	97	GSP1	26.3	5.2	0.735
24,908	8.73	122	RPS5	18.6	NA ^c	0.899
25,081	4.65	81	MRP8	9.3	NA ^c	0.241
25,960	6.06	116	RPE1	5.8	0.7	0.372
26,378	9.55	127	RPS3	96.8	NA ^c	0.863
26,467	5.18	100	VMA4	10.5	3.7	0.427
26,661	5.84	98	TPI1	NA ^d	NA ^c	0.900
27,156	5.56	93	PRE8	6.9	0.7	0.129
27,334	6.13	115	YHR049W	18.4	2.2	0.520
27,472	5.33	92	YNL010W	31.6	3.7	0.421
27,480	8.95	123	GPM1	10.0	169.4	0.902
27,480	8.95	124	GPM1	231.4	169.4	0.902
27,480	8.95	125	GPM1	7.5	169.4	0.902
27,809	5.97	139	HOR2	5.7	0.7	0.381
27,874	4.46	78	YST1	13.6	52.8	0.805
28,595	4.51	41	PUP2	4.4	0.7	0.147
29,156	6.59	114	YMR226C	14.5	2.2	0.283
29,244	8.40	120	DPM1	5.0	11.2	0.362
29,443	5.91	48	PRE4	3.4	3.7	0.162
30,012	6.39	138	PRB1	21.2	1.5	0.449
30,073	4.63	77	BMH1	14.7	28.2	0.454
30,296	7.94	121	OMP2	67.4	41.6	0.499
30,435	6.34	89	GPP1	70.2	11.2	0.703
31,332	5.57	88	ILV6	13.9	3.0	0.402
32,159	5.46	113	IPP1	63.1	3.7	0.752
32,263	6.00	149	HIS1	22.4	4.5	0.232
33,311	5.35	84	SPE3	15.1	6.7	0.468
34,465	5.60	129	ADE1	8.7	5.2	0.305
34,762	5.32	85	SEC14	10.9	6.0	0.373
34,797	5.85	42	URA1	49.5	8.9	0.237
34,799	6.04	90	BEL1	103.2	81.0	0.875
35,556	5.97	43	YDL124W	6.4	4.5	0.206
35,619	8.41	59	TDH1	69.8	32.7 ^e	0.940
35,650	5.49	68	CAR1	5.2	3.0	0.339
35,712	6.72	117	TDH2	49.6	473.0 ^f	0.982
35,712	6.72	154	TDH2	863.5	473.0 ^f	0.982
35,712	6.72	155	TDH2	79.4	473.0 ^f	0.982
36,272	4.85	128	APA1	8.7	0.7	0.425
36,358	5.05	75	YJR105W	17.6	17.1	0.522
36,358	5.05	76	YJR105W	27.5	17.1	0.522
36,596	6.37	79	ADH2	58.9	260.0 ^f	0.711
36,714	6.30	102	ADH1	746.1	260.0	0.913
36,714	6.30	103	ADH1	17.6	260.0	0.913
36,714	6.30	104	ADH1	61.4	260.0	0.913
36,714	6.30	105	ADH1	52.7	260.0	0.913
37,033	6.23	44	TAL1	44.8	3.7	0.701
37,796	7.36	57	IDH2	29.4	6.7	0.330
37,886	6.49	106	ILV5	76.0	4.5	0.892
38,700	7.83	55	BAT1	30.9	11.2	0.469
38,702	6.24	46	QCR2	NA ^d	2.2	0.326

Continued

TABLE 1—Continued

Mol wt	pI	Spot no.	YPD gene name ^a	Protein abundance (10 ³ copies/cell)	mRNA abundance (copies/cell)	Codon bias
39,477	5.58	86	FBA1	17.8	183.6	0.935
39,477	5.58	87	FBA1	427.2	183.6	0.935
39,540	6.50	150	HOM2	60.3	4.5	0.592
39,561	6.12	156	PSA1	96.4	27.5	0.718
41,158	6.01	49	YNL134C	14.9	1.5	0.316
41,623	7.18	58	BAT2	19.0	8.9	0.250
41,728	7.29	110	ERG10	24.1	4.5	0.543
41,900	5.42	74	TOM40	22.3	2.2	0.375
42,402	6.29	45	CYS3	6.7	8.9	0.621
42,883	5.63	67	DYS1	15.8	5.2	0.526
43,409	6.31	107	SER1	10.5	1.5	0.292
43,421	5.59	91	ERG6	2.2	14.1	0.408
44,174	7.32	56	YBR025C	13.1	6.0	0.684
44,682	4.99	72	TIF1	2.9	39.4	0.834
44,707	7.77	108	PGK1	23.7	165.7	0.897
44,707	7.77	109	PGK1	315.2	165.7	0.897
46,080	6.72	30	CAR2	15.4	NA ^c	0.495
46,383	8.52	53	IDP1	7.7	0.7	0.436
46,553	5.98	47	IDP2	32.4	NA ^c	0.197
46,679	6.39	50	ENO1	35.4	0.7	0.930
46,679	6.39	51	ENO1	6.6	0.7	0.930
46,679	6.39	52	ENO1	2.2	0.7	0.930
46,773	5.82	63	ENO2	15.5	289.1	0.960
46,773	5.82	64	ENO2	635.5	289.1	0.960
46,773	5.82	65	ENO2	93.0	289.1	0.960
46,773	5.82	66	ENO2	31.0	289.1	0.960
47,402	6.09	126	COR1	2.5	0.7	0.422
47,666	8.98	54	AAT2	11.7	6.0	0.338
48,364	5.25	73	WTM1	74.5	13.4	0.365
48,530	6.20	61	MET17	38.1	29.0	0.576
48,904	5.18	69	LYS9	16.2	3.7	0.463
48,987	4.90	153	SUP45	29.6	11.9	0.377
49,727	5.47	70	PRO2	13.6	5.2	0.297
49,912	9.27	62	TEF2	558.5	282.0	0.932
50,444	5.67	35	YDR190C	4.8	2.2	0.228
50,837	6.11	32	YEL047C	3.8	1.5	0.387
50,891	4.59	151	TUB2	11.2	7.4	0.404
51,547	6.80	27	LPD1	18.9	2.2	0.351
52,216	7.25	29	SHM2	19.7	7.4	0.722
52,859	5.54	37	YFR044C	30.2	6.7	0.442
53,798	5.19	71	HXK2	26.5	7.4	0.756
53,803	6.05	145	GYP6	4.4	0.7	0.147
54,403	5.29	39	ALD6	37.7	2.2	0.664
54,403	5.29	40	ALD6	6.6	2.2	0.664
54,502	6.20	31	ADE13	6.3	1.5	0.417
54,543	7.75	25	PYK1	225.3	101.8	0.965
54,543	7.75	26	PYK1	39.8	101.8	0.965
55,221	6.66	146	YEL071W	16.3	3.0	0.244
55,295	4.35	134	PDH1	66.2	14.1	0.589
55,364	5.98	24	GLK1	22.6	6.0	0.237
55,481	7.97	118	ATP1	21.6	2.2	0.637
55,886	6.47	28	CYS4	22.2	NA ^c	0.444
56,167	5.83	33	ARO8	14.3	3.0	0.324
56,167	5.83	34	ARO8	9.1	3.0	0.324
56,584	6.36	20	CYB2	18.9	NA ^c	0.259
57,366	5.53	60	FRS2	2.3	0.7	0.451
57,383	5.98	144	ZWF1	5.6	0.7	0.215
57,464	5.49	36	THR4	21.4	3.7	0.508
57,512	5.50	7	SRV2	6.5	NA ^c	0.260
57,727	4.92	152	VMA2	33.7	8.9	0.546
58,573	6.47	17	ACH1	4.4	1.5	0.327
58,573	6.47	18	ACH1	5.4	1.5	0.327
61,353	5.87	21	PDC1	6.5	200.7	0.962
61,353	5.87	22	PDC1	303.2	200.7	0.962
61,353	5.87	23	PDC1	16.3	200.7	0.962
61,649	5.54	38	CCT8	2.2	1.5	0.271

Continued on following page

TABLE 1—Continued

Mol wt	pI	Spot no.	YPD gene name ^a	Protein abundance (10 ³ copies/cell)	mRNA abundance (copies/cell)	Codon bias
61,902	6.21	101	PDC5	4.3	NA ^c	0.828
62,266	6.19	16	ICL1	20.1	NA ^c	0.327
62,862	8.02	19	ILV3	5.3	4.5	0.548
63,082	6.40	119	PGM2	2.2	3.0	0.402
64,335	5.77	5	PAB1	30.4	1.5	0.616
66,120	5.42	8	STI1	6.7	0.7	0.313
66,120	5.42	9	STI1	6.4	0.7	0.313
66,450	5.29	141	SSB2	7.0	NA ^c	0.880
66,450	5.29	142	SSB2	2.3	NA ^c	0.880
66,456	5.23	10	SSB1	64.5	79.5	0.907
66,456	5.23	11	SSB1	59.0	79.5	0.907
66,456	5.23	12	SSB1	13.7	79.5	0.907
68,397	5.82	82	LEU4	3.1	3.0	0.407
69,313	4.90	13	SSA2	24.3	18.6	0.892
69,313	4.90	14	SSA2	77.1	18.6	0.892
74,378	8.46	15	YKL029C	2.8	3.7	0.353
75,396	5.82	6	GRS1	5.5	7.4	0.500
85,720	6.25	1	MET6	2.0	NA ^c	0.772
85,720	6.25	2	MET6	10.9	NA ^c	0.772
85,720	6.25	3	MET6	1.4	NA ^c	0.772
93,276	6.11	131	EFT1	17.9	41.6	0.890
93,276	6.11	132	EFT1	5.7	41.6	0.890
102,064 ^c	6.61 ^c	94	ADE3	4.8	5.2	0.423
107,482 ^c	5.33 ^c	4	MCM3	2.7	NA ^c	0.240

^a YPD gene names are available from the YPD website (39).

^b NA, calculation could not be performed or was not available.

^c mRNA data inconclusive or NA.

^d No methionines in predicted ORF; therefore, protein concentration was not determined.

^e Measured molecular weight or pI did not match theoretical molecular weight or pI.

Protein quantitation. [³⁵S]methionine-labeled gels were exposed to X-ray film overnight, and then the silver stain and film were used to excise 156 spots of varying intensities, molecular weights, and pIs. The excised spots were placed in 0.6-ml microcentrifuge tubes, and scintillation cocktail (100 μ l) was added. The samples were vortexed and counted. In addition, two parallel gels were electroblotted to polyvinylidene difluoride membranes. The membranes were exposed to X-ray film, and four intense single spots were excised from each membrane and subjected to amino acid analysis. For these four spots, a mean of 209 \pm 4 cpm/pmol of protein/methionine was found. This number was used to quantitate all remaining spots in conjunction with the number of methionines present in the protein.

To ensure that proteins were labeled to equilibrium, parallel 2D gels were prepared and run on yeast metabolically labeled for 1, 2, 6, or 18 h. The corresponding 156 spots were excised from each gel, and radioactivity was measured by liquid scintillation counting for each spot. Calculated protein levels were highly reproducible for all time points measured after 1 h.

Calculation of codon bias and predicted half-life. Codon bias values were extracted from the YPD spreadsheet (17). Protein half-lives were calculated based on the N-end rule (33). When the N-terminal processing was not known experimentally, it was predicted based on the affinity of methionine aminopeptidase (31).

RESULTS

Characteristics of proteome approach. Nearly every facet of proteome analysis hinges on the unambiguous identification of large numbers of expressed proteins in cells. Several techniques have been described previously for the identification of proteins separated by 2DE, including N-terminal and internal sequencing (1, 2), amino acid analysis (38), and more recently mass spectrometry (25). We utilized techniques based on mass spectrometry because they afford the highest levels of sensitivity and provide unambiguous identification. The specific procedure used is schematically illustrated in Fig. 1 and is based on three principles. First, proteins are removed from the gel by

proteolytic in-gel digestion, and the resulting peptides are separated by on-line capillary high-performance liquid chromatography. Second, the eluting peptides are ionized and detected, and the specific peptide ions are selected and fragmented by the mass spectrometer. To achieve this, the mass spectrometer switches between the MS mode (for peptide mass identification) and the MS/MS mode (for peptide characterization and sequencing). Selected peptides are fragmented by a process called collision-induced dissociation (CID) to generate a tandem mass spectrum (MS/MS spectrum) that contains the peptide sequence information. Third, individual CID mass spectra are then compared by computer algorithms to predicted spectra from a sequence database. This results in the identification of the peptide and, by association, the protein(s) in the spot. Unambiguous protein identification is attained in a single analysis by the detection of multiple peptides derived from the same protein.

Protein identification. Yeast total cell protein lysate (40 μ g), metabolically labeled with [³⁵S]methionine, was electrophoretically separated by isoelectric focusing in the first dimension and by SDS-10% polyacrylamide gel electrophoresis in the second dimension. Proteins were visualized by silver staining and by autoradiography. Of the more than 1,000 proteins visible by silver staining, 156 spots were excised from the gel and subjected to in-gel tryptic digestion, and the resulting peptides were analyzed and identified by microspray LC-MS/MS techniques as described above. The proteins in this study were all identified automatically by computer software with no human interpretation of mass spectra. They are indicated in Fig. 2 and detailed in Table 1.

The CID spectra shown in Fig. 3 indicate that the quality of the identification data generated was suitable for unambiguous protein identification. The spectra represent the amino acid sequences of tryptic peptides NSGDIVNLGSIAGR (Fig. 3A) and FAVGAFTDSLRL (Fig. 3B). Both peptides were derived from protein S57593 (hypothetical protein YMR226C), which migrated to spot 114 (molecular weight, 29,156; pI, 6.59) in the 2D gel in Fig. 2. Five other peptides from the same analysis were also computer matched to the same protein sequence.

Protein and mRNA quantitation. For the 156 genes investigated, the protein expression levels ranged from 2,200 (PGM2) to 863,000 (TDH2/TDH3) copies/cell. The levels of mRNA for each of the genes identified were calculated from SAGE frequency tables (35). These tables contain the mRNA levels for 4,665 genes in yeast strain YPH499 grown to mid-log phase in YPD medium on glucose as a carbon source. In some instances, the mRNA levels could not be calculated for reasons stated in Materials and Methods. For the proteins analyzed in this study, mean transcript levels varied from 0.7 to 473 copies/cell.

Selection of the sample population for mRNA-protein expression level correlation. The protein spots selected for identification were selected from spots visible by silver staining in the 2D gel. An attempt was made not to include spots where overlap with other spots was readily apparent. The number of proteins identified was 156 (Table 1). Some proteins migrated to more than one spot (presumably due to differential protein processing or modifications), and protein levels from these spots were calculated by integrating the intensities of the different spots. The 156 protein spots analyzed represented the products of 128 different genes. Genes were excluded from the correlation analysis only if part of the data set was missing; i.e., genes were excluded if (i) no mRNA expression data were available for the protein or putative SAGE tags were ambiguous, (ii) the amino acid sequence did not contain methionine, (iii) more than a single protein was conclusively identified as

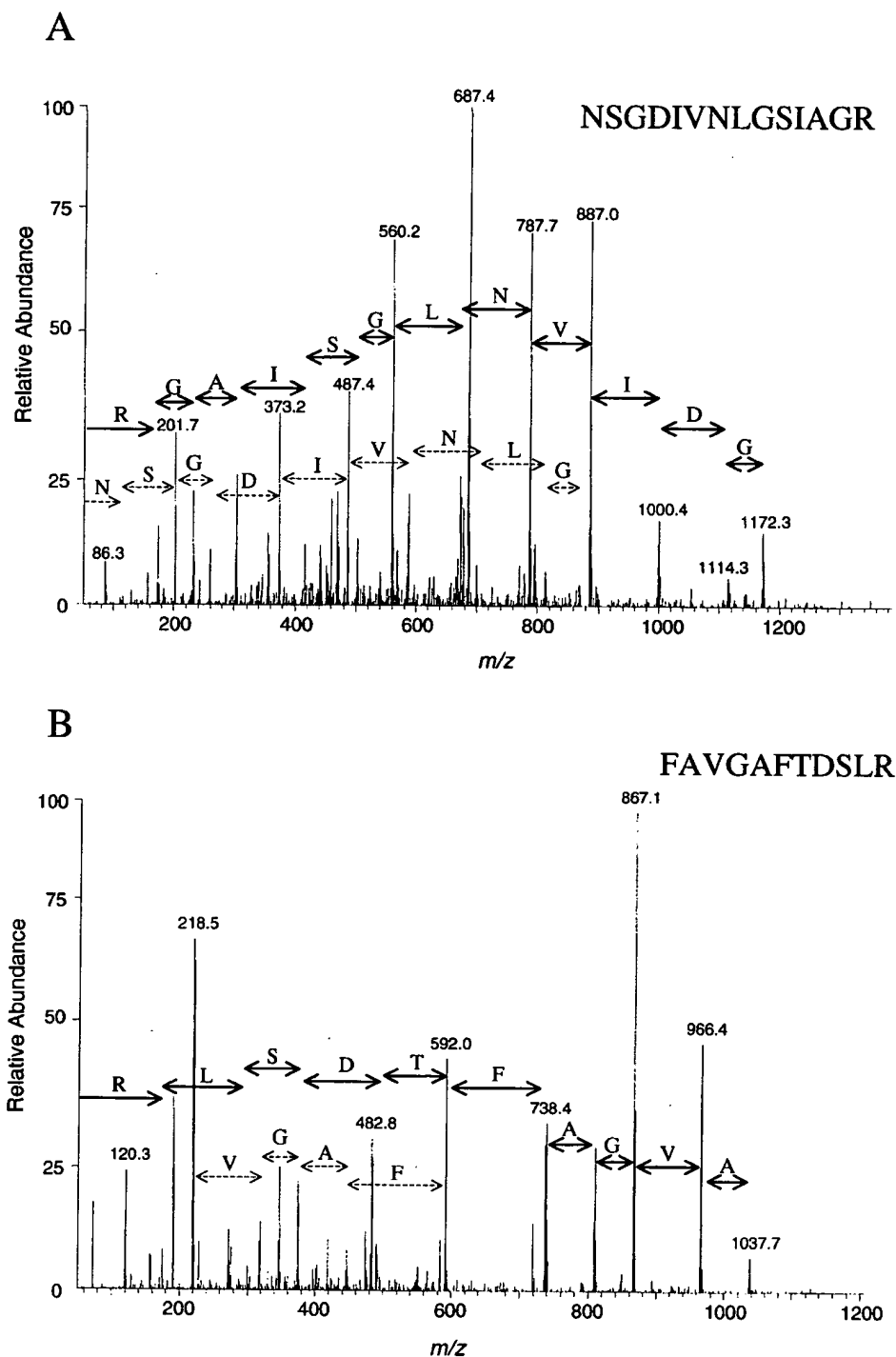


FIG. 3. Tandem mass (MS/MS) spectra resulting from analysis of a single spot on a 2D gel. The first quadrupole selected a single mass-to-charge ratio (m/z) of 687.2 (A) or 592.6 (B), while the collision cell was filled with argon gas, and a voltage which caused the peptide to undergo fragmentation by CID was applied. The third quadrupole scanned the mass range from 50 to 1,400 m/z . The computer program Sequest (8) was utilized to match MS/MS spectra to amino acid sequence by database searching. Both spectra matched peptides from the same protein, S57593 (yeast hypothetical protein YMR226C). Five other peptides from the same analysis were matched to the same protein.

migrating to the same gel spot, or (iv) the theoretical and observed pIs and molecular weights could not be reconciled. After these criteria were applied, the number of genes used in the correlation analysis was 106.

Codon bias and predicted half-lives. Codon bias is thought to be an indicator of protein expression, with highly expressed proteins having large codon bias values. The codon bias distribution for the entire set of more than 6,000 predicted yeast

gene ORFs is presented in Fig. 4A. The interval with the largest frequency of genes is between the codon bias values of 0.0 and 0.1. This segment contains more than 2,500 genes. The distribution of the codon bias values of the 128 different genes found in this study (all protein spots from Fig. 2) is shown in Fig. 4B, and protein half-lives (predicted from applying the N-end rule [33] to the experimentally determined or predicted protein N termini) are shown in Fig. 4C. No genes were identified with codon bias values less than 0.1 even though thousands of genes exist in this category. In addition, nearly all of the proteins identified had long predicted half-lives (greater than 30 h).

Correlation of mRNA and protein expression levels. The correlation between mRNA and protein levels of the genes selected as described above is shown in Fig. 5. For the entire group (106 genes) for which a complete data set was generated, there was a general trend of increased protein levels resulting from increased mRNA levels. The Pearson product moment correlation coefficient for the whole data set (106 genes) was 0.935. This number is highly biased by a small number of genes with very large protein and message levels. A more representative subset of the data is shown in the inset of Fig. 5. It shows genes for which the message level was below 10 copies/cell and includes 69% (73 of 106 genes) of the data used in the study. The Pearson product moment correlation coefficient for this data set was only 0.356. We also found that levels of protein expression coded for by mRNA with comparable abundance varied by as much as 30-fold and that the mRNA levels coding for proteins with comparable expression levels varied by as much as 20-fold.

The distortion of the correlation value induced by the uneven distribution of the data points along the *x* axis is further demonstrated by the analysis in Fig. 6. The 106 samples included in the study were ranked by protein abundance, and the Pearson product moment correlation coefficient was repeatedly calculated after including progressively more, and higher-abundance, proteins in each calculation. The correlation values remained relatively stable in the range of 0.1 to 0.4 if the lowest-expressed 40 to 95 proteins used in this study were included. However, the correlation value steadily climbed by the inclusion of each of the 11 very highly expressed proteins.

Correlation of protein and mRNA expression levels with codon bias. Codon bias is the propensity for a gene to utilize the same codon to encode an amino acid even though other codons would insert the identical amino acid in the growing polypeptide sequence. It is further thought that highly expressed proteins have large codon biases (3). To assess the value of codon bias for predicting mRNA and protein levels in exponentially growing yeast cells, we plotted the two experimental sets of data versus the codon bias (Fig. 7). The distribution patterns for both mRNA and protein levels with respect to codon bias were highly similar. There was high variability in the data within the codon bias range of 0.8 to 1.0. Although a large codon bias generally resulted in higher protein and message expression levels, codon bias did not appear to be predictive of either protein levels or mRNA levels in the cell.

DISCUSSION

The desired end point for the description of a biological system is not the analysis of mRNA transcript levels alone but also the accurate measurement of protein expression levels and their respective activities. Quantitative analysis of global mRNA levels currently is a preferred method for the analysis of the state of cells and tissues (11). Several methods which either provide absolute mRNA abundance (34, 35) or relative

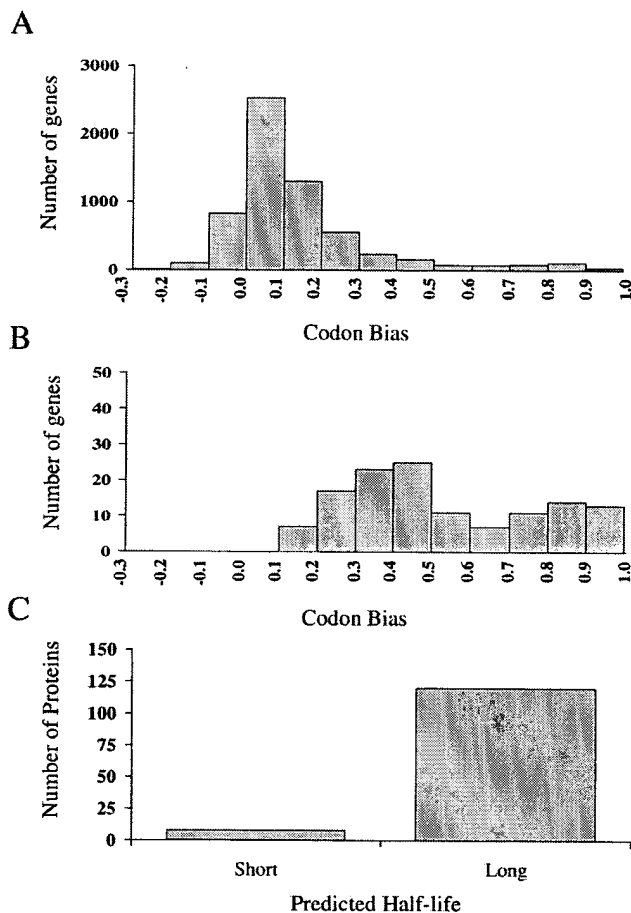


FIG. 4. Current proteome analysis technology utilizing 2DE without pre-enrichment samples mainly highly expressed and long-lived proteins. Genes encoding highly expressed proteins generally have large codon bias values. (A) Distribution of the yeast genome (more than 6,000 genes) based on codon bias. The interval with the largest frequency of genes is 0.0 to 0.1, with more than 2,500 genes. (B) Distribution of the genes from identified proteins in this study based on codon bias. No genes with codon bias values less than 0.1 were detected in this study. (C) Distribution of identified proteins in this study based on predicted half-life (estimated by N-end rule).

mRNA levels in comparative analyses (20, 27) have been described elsewhere. The techniques are fast and exquisitely sensitive and can provide mRNA abundance for potentially any expressed gene. Measured mRNA levels are often implicitly or explicitly extrapolated to indicate the levels of activity of the corresponding protein in the cell. Quantitative analysis of protein expression levels (proteome analysis) is much more time-consuming because proteins are analyzed sequentially one by one and is not general because analyses are limited to the relatively highly expressed proteins. Proteome analysis does, however, provide types of data that are of critical importance for the description of the state of a biological system and that are not readily apparent from the sequence and the level of expression of the mRNA transcript. This study attempts to examine the relationship between mRNA and protein expression levels for a large number of expressed genes in cells representing the same state.

Limits in the sensitivity of current protein analysis technology precluded a completely random sampling of yeast proteins. We therefore based the study on those proteins visible by silver

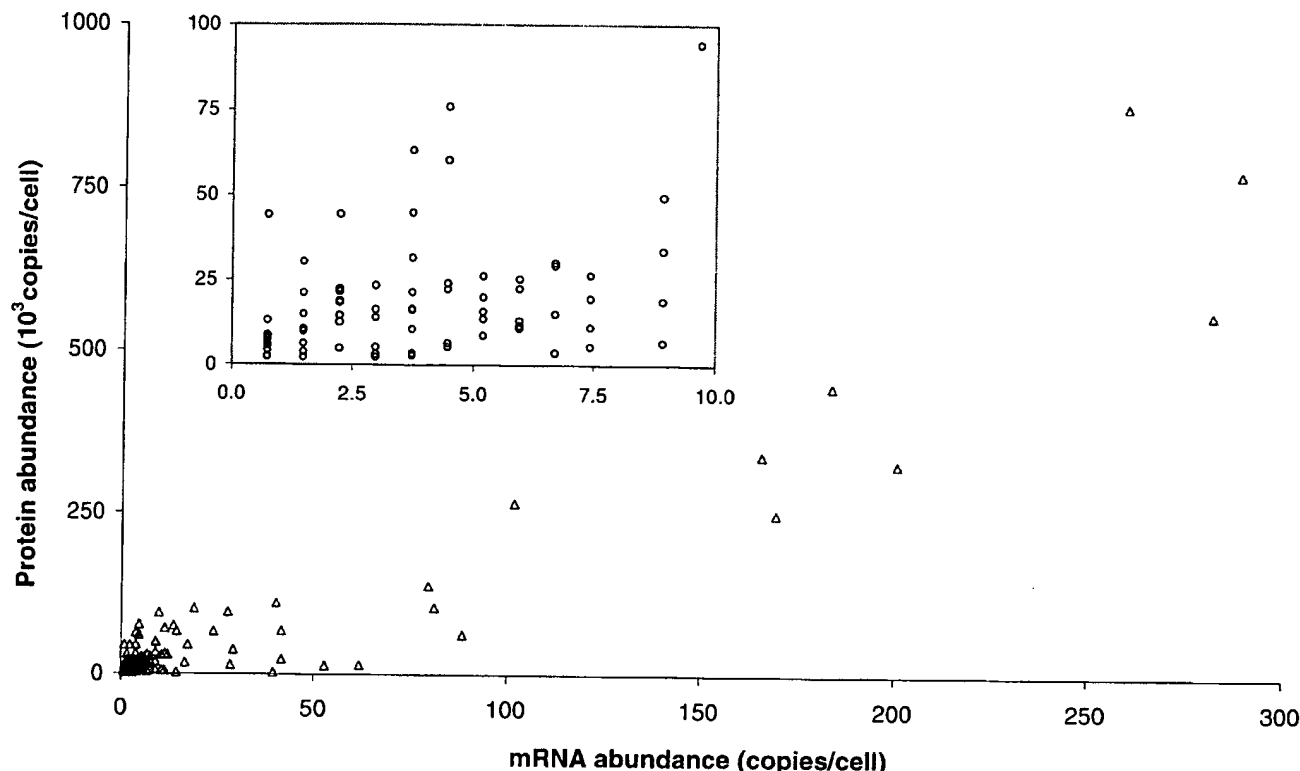


FIG. 5. Correlation between protein and mRNA levels for 106 genes in yeast growing at log phase with glucose as a carbon source. mRNA and protein levels were calculated as described in Materials and Methods. The data represent a population of genes with protein expression levels visible by silver staining on a 2D gel chosen to include the entire range of molecular weights, isoelectric focusing points, and staining intensities. The inset shows the low-end portion of the main figure. It contains 69% of the original data set. The Pearson product moment correlation for the entire data set was 0.935. The correlation for the inset containing 73 proteins (69%) was only 0.356.

staining on a 2D gel. Of the more than 1,000 visible spots, 156 were chosen to include the entire range of molecular weights, isoelectric focusing points, and staining intensities displayed on the 2D protein pattern. The genes identified in this study shared a number of properties. First, all of the proteins in this study had a codon bias of greater than 0.1 and 93% were greater than 0.2 (Fig. 4B). Second, with few exceptions, the proteins in this study had long predicted half-lives according to the N-end rule (Fig. 4C). Third, low-abundance proteins with regulatory functions such as transcription factors or protein kinases were not identified.

Because the population of proteins used in this study appears to be fairly homogeneous with respect to predicted half-life and codon bias, it might be expected that the correlation of the mRNA and protein expression levels would be stronger for this population than for a random sample of yeast proteins. We tested this assumption by evaluating the correlation value if different subsets of the available data were included in the calculation. The 106 proteins were ranked from lowest to highest protein expression level, and the trend in the correlation value was evaluated by progressively including more of the higher-abundance proteins in the calculation (Fig. 6). The correlation value when only the lower-abundance 40 to 93 proteins were examined was consistently between 0.1 and 0.4. If the 11 most abundant proteins were included, the correlation steadily increased to 0.94. We therefore expect that the correlation for all yeast proteins or for a random selection would be less than 0.4. The observed level of correlation between mRNA and protein expression levels suggests the importance

of posttranslational mechanisms controlling gene expression. Such mechanisms include translational control (15) and control of protein half-life (33). Since these mechanisms are also active in higher eukaryotic cells, we speculate that there is no predictive correlation between steady-state levels of mRNA and those of protein in mammalian cells.

Like other large-scale analyses, the present study has several potential sources of error related to the methods used to determine mRNA and protein expression levels. The mRNA levels were calculated from frequency tables of SAGE data. This method is highly quantitative because it is based on actual sequencing of unique tags from each gene, and the number of times that a tag is represented is proportional to the number of mRNA molecules for a specific gene. This method has some limitations including the following: (i) the magnitude of the error in the measurement of mRNA levels is inversely proportional to the mRNA levels, (ii) SAGE tags from highly similar genes may not be distinguished and therefore are summed, (iii) some SAGE tags are from sequences in the 3' untranslated region of the transcript, (iv) incomplete cleavage at the SAGE tag site by the restriction enzyme can result in two tags representing one mRNA, and (v) some transcripts actually do not generate a SAGE tag (34, 35).

For the SAGE method, the error associated with a value increases with a decreasing number of transcripts per cell. The conclusions drawn from this study are dependent on the quality of the mRNA levels from previously published data (35). Since more than 65% of the mRNA levels included in this study were calculated to 10 copies/cell or less (40% were less

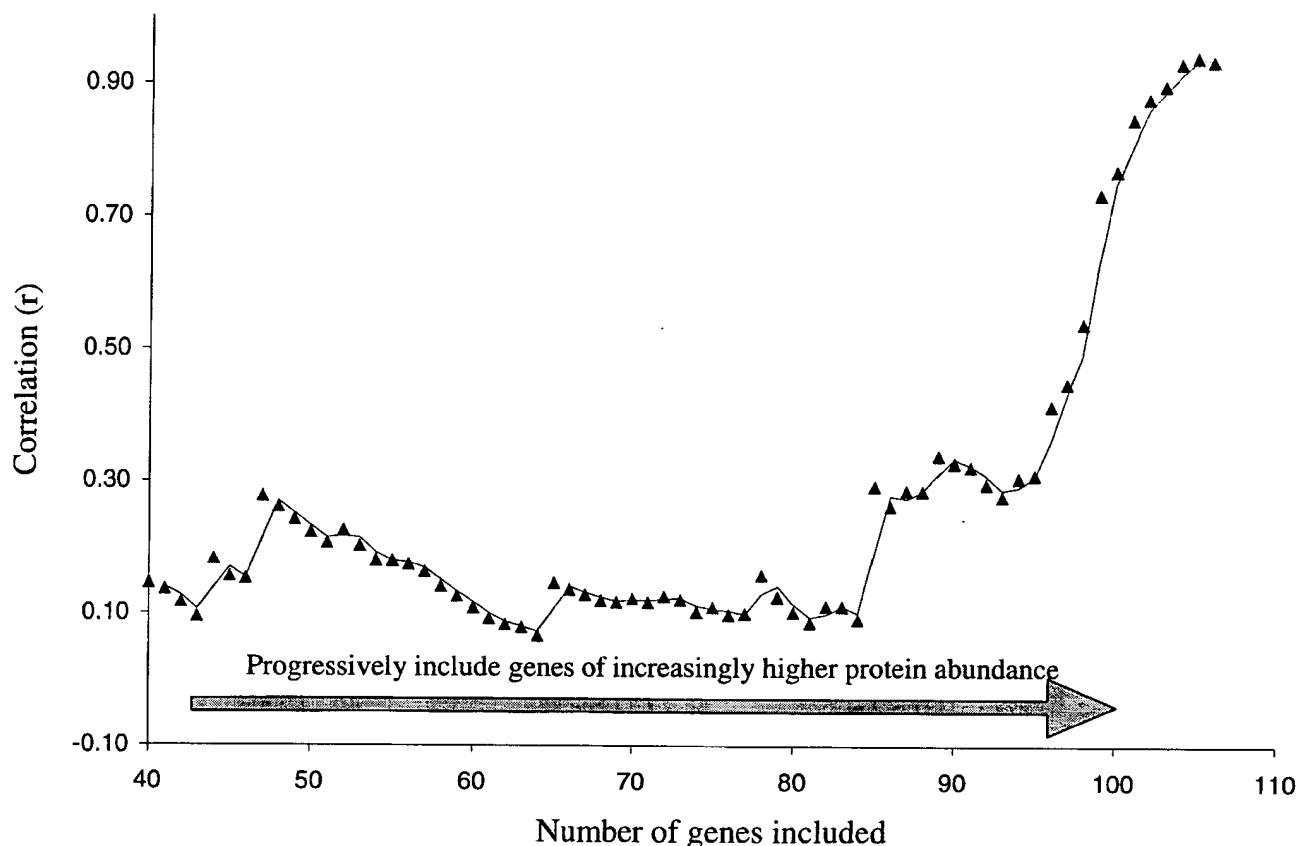


FIG. 6. Effect of highly abundant proteins on Pearson product moment correlation coefficient for mRNA and protein abundance in yeast. The set of 106 genes was ranked according to protein abundance, and the correlation value was calculated by including the 40 lowest-abundance genes and then progressively including the remaining 66 genes in order of abundance. The correlation value climbs as the final 11 highly abundant proteins are included.

than 4 copies/cell), the error associated with these values may be quite large. The mRNA levels were calculated from more than 20,000 transcripts. Assuming that the estimate of 15,000 mRNA molecules per cell is correct (16), this would mean that mRNA transcripts present at only a single copy per cell would be detected 72% of the time (35). The mRNA levels for each gene were carefully scrutinized, and only mRNA levels for which a high degree of confidence existed were included in the correlation value.

Protein abundance was determined by metabolic radiolabeling with [^{35}S]methionine. The calculation required knowledge of three variables: the number of methionines in the mature protein, the radioactivity contained in the protein, and the specific activity of the radiolabel normalized per methionine. The number of methionines per protein was determined from the amino acid sequence of the proteins identified by tandem mass spectrometry. For some proteins, it was not known whether the methionine of the nascent polypeptide was processed away. The N termini of those proteins were predicted based on the specificity of methionine aminopeptidase (31). If the N-terminal processing did not conform to the predicted specificity of processing enzymes, the calculation of the number of methionines would be affected. This discrepancy would affect most the quantitation of a protein with a very low number of methionines. The average number of calculated methionines per protein in this study was 7.2. We therefore expect the potential for erroneous protein quantitation due to unusual N-terminal processing to be small.

The amount of radioactivity contained in a single spot might be the sum of the radioactivity of comigrating proteins. Because protein identification was based on tandem mass spectrometric techniques, comigrating proteins could be identified. However, comigrating proteins were rarely detected in this study, most likely because relatively small amounts of total protein (40 μg) were initially loaded onto the gels, which resulted in highly focused spots containing generally 1 to 25 ng of protein. Because of the relatively small amount loaded, the concentrations of any potentially comigrating protein would likely be below the limit of detection of the mass spectrometry technique used in this study (1 to 5 ng) and below the limit of visualization by silver staining (1 to 5 ng). In the overwhelming majority of the samples analyzed, numerous peptides from a single protein were detected. It is assumed that any comigrating proteins were at levels too low to be detected and that their influence in the calculation would be small.

The specific activity of the radiolabel was determined by relating the precise amount of protein present in selected spots of a parallel gel, as determined by quantitative amino acid composition analysis, to the number of methionines present in the sequence of those proteins and the radioactivity determined by liquid scintillation counting. It is possible that the resulting number might be influenced by unavoidable losses inherent in the amino acid analysis procedure applied. Because four different proteins were utilized in the calculation and the experiment was done in duplicate, the specific activity calculated is thought to be highly accurate. Indeed, the specific

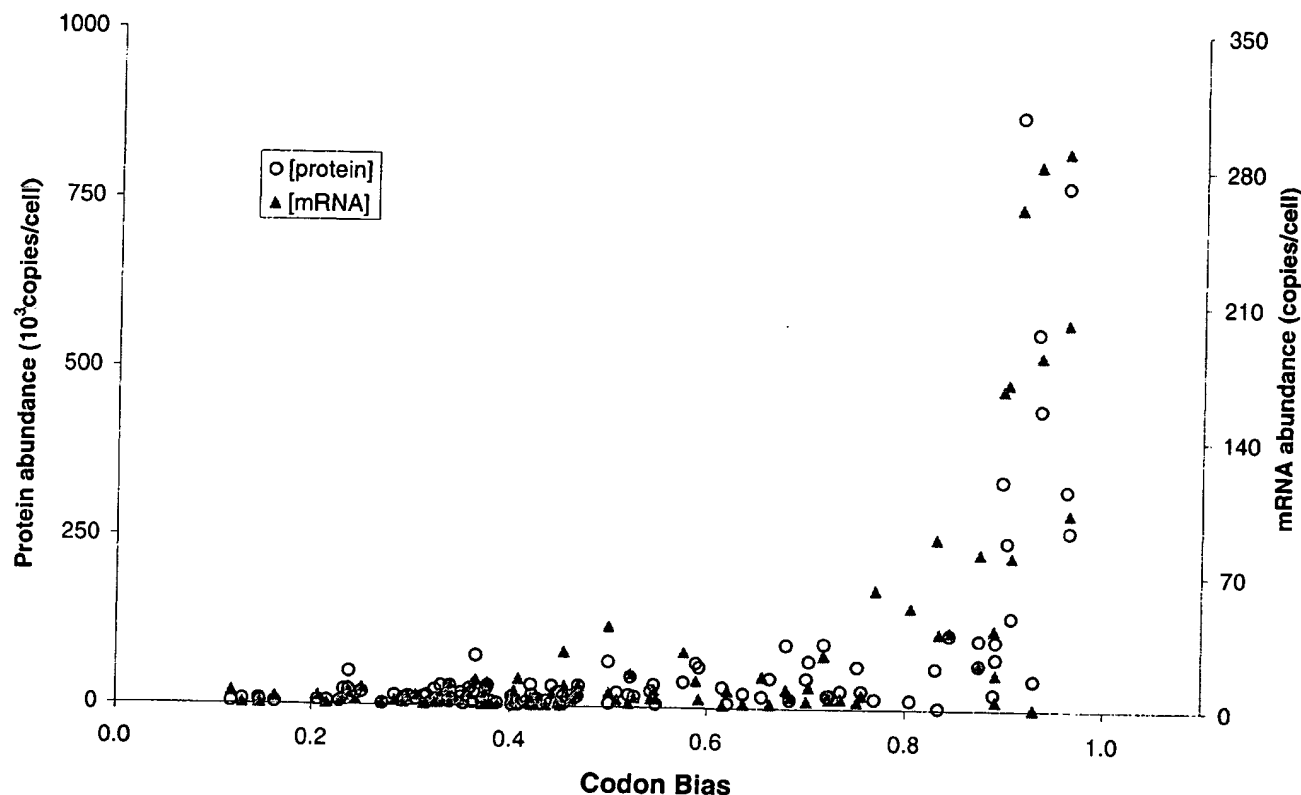


FIG. 7. Relationship between codon bias and protein and mRNA levels in this study. Yeast mRNA and protein expression levels were calculated as described in Materials and Methods. The data represent the same 106 genes as in Fig. 5.

activities calculated for each of the four proteins varied by less than 10%. Any inconsistencies in the calculation of the specific activity would result in differences in the absolute levels calculated but not in the relative numbers and would therefore not influence the correlation value determined.

The protein quantitative method used eliminates a number of potential errors inherent in previous methods for the quantitation of proteins separated by 2DE, such as preferential protein staining and bias caused by inequalities in the number of radiolabeled residues per protein. Any 2D gel-based method of quantitation is complicated by the fact that in some cases the translation products of the same mRNA migrated to different spots. One major reason is posttranslational modification or processing of the protein. Also, artifactual proteolysis during cell lysis and sample preparation can lead to multiple resolved forms of the protein. In such cases, the protein levels of spots coded for by the same mRNA were pooled. In addition, the existence of other spots coded for by the same mRNA that were not analyzed by mass spectrometry or that were below the limit of detection for silver staining cannot be ruled out. However, since this study is based on a class of highly expressed proteins, the presence of undetected minor spots below silver staining sensitivity corresponding to a protein analyzed in the study would generally cause a relatively small error in protein quantitation.

Codon bias is a measure of the propensity of an organism to selectively utilize certain codons which result in the incorporation of the same amino acid residue in a growing polypeptide chain. There are 61 possible codons that code for 20 amino acids. The larger the codon bias value, the smaller the number of codons that are used to encode the protein (19). It is

thought that codon bias is a measure of protein abundance because highly expressed proteins generally have large codon bias values (3, 13).

Nearly all of the most highly expressed proteins had codon bias values of greater than 0.8. However, we detected a number of genes with high codon bias and relative low protein abundance (Fig. 7). For example, the expressed gene with both the second largest protein and mRNA levels in the study was ENO2_YEAST (775,000 and 289.1 copies/cell, respectively). ENO1_YEAST was also present in the gel at much lower protein and mRNA levels (44,200 and 0.7 copies/cell, respectively). The codon bias values for ENO2 and ENO1 are similar (0.96 and 0.93, respectively), but the expression of the two genes is differentially regulated. Specifically, ENO1_YEAST is glucose repressed (6) and was therefore present in low abundance under the conditions used. Other genes with large codon bias values that were not of high protein abundance in the gel include EFT1, TIF1, HXK2, GSP1, EGD2, SHM2, and TAL1. We conclude that merely determining the codon bias of a gene is not sufficient to predict its protein expression level.

Interestingly, codon bias appears to be an excellent indicator of the boundaries of current 2D gel proteome analysis technology. There are thousands of genes with expressed mRNA and likely expressed protein with codon bias values less than 0.1 (Fig. 4A). In this study, we detected none of them, and only a very small percentage of the genes detected in this study had codon bias values between 0.1 and 0.2 (Fig. 4B). Indeed, in every examined yeast proteome study (5, 7, 13, 28) where the combined total number of identified proteins is 300 to 400, this same observation is true. It is expected that for the more complex cells of higher eukaryotic organisms the detection of

low-abundance proteins would be even more challenging than for yeast. This indicates that highly abundant, long-lived proteins are overwhelmingly detected in proteome studies. If proteome analysis is to provide truly meaningful information about cellular processes, it must be able to penetrate to the level of regulatory proteins, including transcription factors and protein kinases. A promising approach is the use of narrow-range focusing gels with immobilized pH gradients (IPG) (23). This would allow for the loading of significantly more protein per pH unit covered and also provide increased resolution of proteins with similar electrophoretic mobilities. A standard pH gradient in an isoelectric focusing gel covers a 7-pH-unit range (pH 3 to 10) over 18 cm. A narrow-range focusing gel might expand the range to 0.5 pH units over 18 cm or more. This could potentially increase by more than 10-fold the number of proteins that can be detected. Clearly, current proteome technology is incapable of analyzing low-abundance regulatory proteins without employing an enrichment method for relatively low-abundance proteins. In conclusion, this study examined the relationship between yeast protein and message levels and revealed that transcript levels provide little predictive value with respect to the extent of protein expression.

ACKNOWLEDGMENTS

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Exhibit 3

DECLARATION OF PAUL POLAKIS, Ph.D.

I, Paul Polakis, Ph.D., declare and say as follows:

1. I was awarded a Ph.D. by the Department of Biochemistry of the Michigan State University in 1984. My scientific Curriculum Vitae is attached to and forms part of this Declaration (Exhibit A).
2. I am currently employed by Genentech, Inc. where my job title is Staff Scientist. Since joining Genentech in 1999, one of my primary responsibilities has been leading Genentech's Tumor Antigen Project, which is a large research project with a primary focus on identifying tumor cell markers that find use as targets for both the diagnosis and treatment of cancer in humans.
3. As part of the Tumor Antigen Project, my laboratory has been analyzing differential expression of various genes in tumor cells relative to normal cells. The purpose of this research is to identify proteins that are abundantly expressed on certain tumor cells and that are either (i) not expressed, or (ii) expressed at lower levels, on corresponding normal cells. We call such differentially expressed proteins "tumor antigen proteins". When such a tumor antigen protein is identified, one can produce an antibody that recognizes and binds to that protein. Such an antibody finds use in the diagnosis of human cancer and may ultimately serve as an effective therapeutic in the treatment of human cancer.
4. In the course of the research conducted by Genentech's Tumor Antigen Project, we have employed a variety of scientific techniques for detecting and studying differential gene expression in human tumor cells relative to normal cells, at genomic DNA, mRNA and protein levels. An important example of one such technique is the well known and widely used technique of microarray analysis which has proven to be extremely useful for the identification of mRNA molecules that are differentially expressed in one tissue or cell type relative to another. In the course of our research using microarray analysis, we have identified approximately 200 gene transcripts that are present in human tumor cells at significantly higher levels than in corresponding normal human cells. To date, we have generated antibodies that bind to about 30 of the tumor antigen proteins expressed from these differentially expressed gene transcripts and have used these antibodies to quantitatively determine the level of production of these tumor antigen proteins in both human cancer cells and corresponding normal cells. We have then compared the levels of mRNA and protein in both the tumor and normal cells analyzed.
5. From the mRNA and protein expression analyses described in paragraph 4 above, we have observed that there is a strong correlation between changes in the level of mRNA present in any particular cell type and the level of protein

expressed from that mRNA in that cell type. In approximately 80% of our observations we have found that increases in the level of a particular mRNA correlates with changes in the level of protein expressed from that mRNA when human tumor cells are compared with their corresponding normal cells.

6. Based upon my own experience accumulated in more than 20 years of research, including the data discussed in paragraphs 4 and 5 above and my knowledge of the relevant scientific literature, it is my considered scientific opinion that for human genes, an increased level of mRNA in a tumor cell relative to a normal cell typically correlates to a similar increase in abundance of the encoded protein in the tumor cell relative to the normal cell. In fact, it remains a central dogma in molecular biology that increased mRNA levels are predictive of corresponding increased levels of the encoded protein. While there have been published reports of genes for which such a correlation does not exist, it is my opinion that such reports are exceptions to the commonly understood general rule that increased mRNA levels are predictive of corresponding increased levels of the encoded protein.

7. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

Dated: 5/07/04

By: Paul Polakis
Paul Polakis, Ph.D.

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Exhibit 2

GNE.3230R1C39

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant	:	Eaton, et al.
Appl. No.	:	10/063,557
Filed	:	May 2, 2002
For	:	SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
Examiner	:	David J. Blanchard
Group Art Unit	:	1642

DECLARATION OF J. CHRISTOPHER GRIMALDI, UNDER 37 C.F.R. § 1.132

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Sir:

I, J. Christopher Grimaldi, declare and say as follows:

1. I am a Senior Research Associate in the Molecular Biology Department of Genentech, Inc., South San Francisco, CA 94080.
2. I joined Genentech in January of 1999. From 1999 to 2003, I directed the Cloning Laboratory in the Molecular Biology Department. During this time I directed or performed numerous molecular biology techniques including qualitative Polymerase Chain Reaction (PCR) analyses. I am currently involved in, among other projects, the isolation of genes coding for membrane associated proteins which can be used as targets for antibody therapeutics against cancer. In connection with the above-identified patent application, I personally performed or directed the semi-quantitative PCR analyses in the assay entitled "Tumor Versus Normal Differential Tissue Expression Distribution" which is described in EXAMPLE 18 in the specification that were used to identify differences in gene expression between tumor tissue and their normal counterparts.
3. My scientific Curriculum Vitae, including my list of publications, is attached to and forms part of this Declaration (Exhibit A).
4. In differential gene expression studies, one looks for genes whose expression levels differ significantly under different conditions, for example, in normal versus diseased tissue.

Appl. No. : 10/063,557
Filed : May 2, 2002

Chromosomal aberrations, such as gene amplification, and chromosomal translocations are important markers of specific types of cancer and lead to the aberrant expression of specific genes and their encoded polypeptides, including over-expression and under-expression. For example, gene amplification is a process in which specific regions of a chromosome are duplicated, thus creating multiple copies of certain genes that normally exist as a single copy. Gene under-expression can occur when a gene is not transcribed into mRNA. In addition, chromosomal translocations occur when two different chromosomes break and are rejoined to each other chromosome resulting in a chimeric chromosome which displays a different expression pattern relative to the parent chromosomes. Amplification of certain genes such as Her2/Neu [Singleton *et al.*, Pathol. Annu., 27Pt1:165-190], or chromosomal translocations such as t(5;14), [Grimaldi *et al.*, Blood, 73(8):2081-2085(1989); Meeker *et al.*, Blood, 76(2):285-289(1990)] give cancer cells a growth or survival advantage relative to normal cells, and might also provide a mechanism of tumor cell resistance to chemotherapy or radiotherapy. When the chromosomal aberration results in the aberrant expression of a mRNA and the corresponding gene product (the polypeptide), as it does in the aforementioned cases, the gene product is a promising target for cancer therapy, for example, by the therapeutic antibody approach.

5. Comparison of gene expression levels in normal versus diseased tissue has important implications both diagnostically and therapeutically. For example, those who work in this field are well aware that in the vast majority of cases, when a gene is over-expressed, as evidenced by an increased production of mRNA, the gene product or polypeptide will also be over-expressed. It is unlikely that one identifies increased mRNA expression without associated increased protein expression. This same principle applies to gene under-expression. When a gene is under-expressed, the gene product is also likely to be under-expressed. Stated in another way, two cell samples which have differing mRNA concentrations for a specific gene are expected to have correspondingly different concentration of protein for that gene. Techniques used to detect mRNA, such as Northern Blotting, Differential Display, *in situ* hybridization, quantitative PCR, Taqman, and more recently Microarray technology all rely on the dogma that a change in mRNA will represent a similar change in protein. If this dogma did not hold true then these techniques would have little value and not be so widely used. The use of mRNA quantitation techniques have identified a seemingly endless number of genes which are differentially expressed in various tissues and these genes have subsequently been shown to have correspondingly similar changes in their protein levels. Thus, the detection of increased mRNA expression is expected to result in increased polypeptide expression, and the detection of decreased mRNA expression is expected to result in decreased polypeptide expression. The detection of increased or decreased polypeptide expression can be used for cancer diagnosis and treatment.

6. However, even in the rare case where the protein expression does not correlate with the mRNA expression, this still provides significant information useful for cancer diagnosis and treatment. For example, if over- or under-expression of a gene product does not correlate with over- or under-expression of mRNA in certain tumor types but does so in others, then identification of both gene expression and protein expression enables more accurate tumor classification and hence better determination of suitable therapy. In addition, absence of over- or

Appl. No. : 10/063,557
Filed : May 2, 2002

under-expression of the gene product in the presence of a particular over- or under-expression of mRNA is crucial information for the practicing clinician. For example, if a gene is over-expressed but the corresponding gene product is not significantly over-expressed, the clinician accordingly will decide not to treat a patient with agents that target that gene product.

7. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

By: _____

J. Christopher Grimaldi

Date: _____

8/10/2001

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The t(5;14) Chromosomal Translocation in a Case of Acute Lymphocytic Leukemia Joins the Interleukin-3 Gene to the Immunoglobulin Heavy Chain Gene

By J. Christopher Grimaldi and Timothy C. Meeker

Chromosomal translocations have proven to be important markers of the genetic abnormalities central to the pathogenesis of cancer. By cloning chromosomal breakpoints one can identify activated proto-oncogenes. We have studied a case of B-lineage acute lymphocytic leukemia (ALL) that was associated with peripheral blood eosinophilia. The chromosomal translocation t(5;14) (q31;q32) from this sample was cloned and studied at the molecular level. This

translocation joined the immunoglobulin heavy chain joining (Jh) region to the promoter region of the interleukin-3 (IL-3) gene in opposite transcriptional orientations. The data suggest that activation of the IL-3 gene by the enhancer of the immunoglobulin heavy chain gene may play a central role in the pathogenesis of this leukemia and the associated eosinophilia.

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KARYOTYPIC STUDIES of leukemia and lymphoma have identified frequent nonrandom chromosomal translocations. Some of these translocations juxtapose the immunoglobulin heavy chain (IgH) gene with important

protooncogenes, such as *c-myc* and *bcl-2*.^{1,2} In this way, the IgH gene can activate proto-oncogenes, resulting in disordered gene expression and a step in the development of cancer. The investigation of additional nonrandom translocations into the IgH locus allows us to identify new genes promoting the generation of leukemia and lymphoma.

A distinct subtype of acute lymphocytic leukemia (ALL) has been characterized by B-lineage phenotype, associated eosinophilia in the peripheral blood, and a t(5;14)(q31;q32) chromosomal translocation.^{3,4} This syndrome probably occurs in <1% of all patients with ALL. We hypothesized that the cloning of the translocation characteristic of this leukemia might allow the identification of an important gene on chromosome 5 that plays a role in the evolution of this disease. In this report we demonstrate that the interleukin-3 gene (IL-3) and the IgH gene are joined by this translocation.

MATERIALS AND METHODS

Sample and DNA blots. A bone marrow aspirate from a representative patient with ALL (L1 morphology by French-American-British [FAB] criteria), peripheral eosinophilia (up to 20,000 per microliter with a normal value of <350 per microliter) and a t(5;14)(q31;q32) translocation was studied. Using published methods, genomic DNA was isolated and DNA blots were made.⁵ Briefly, 10 µg of high molecular weight (mol wt) DNA were digested using an appropriate restriction enzyme and electrophoresed on a 0.8% agarose gel. The gel was stained with ethidium bromide, photographed, denatured, neutralized, and transferred to Hybond (Amersham, Arlington Heights, IL). After treatment of the filter with ultraviolet light, hybridization was performed. The filter was washed to a final stringency of 0.2% saturated sodium citrate (SSC) and 0.1% sodium lauryl sulfate (SDS) and exposed to film. The human Jh probe has been previously reported.⁶

Genomic library. The genomic library was made using pub-

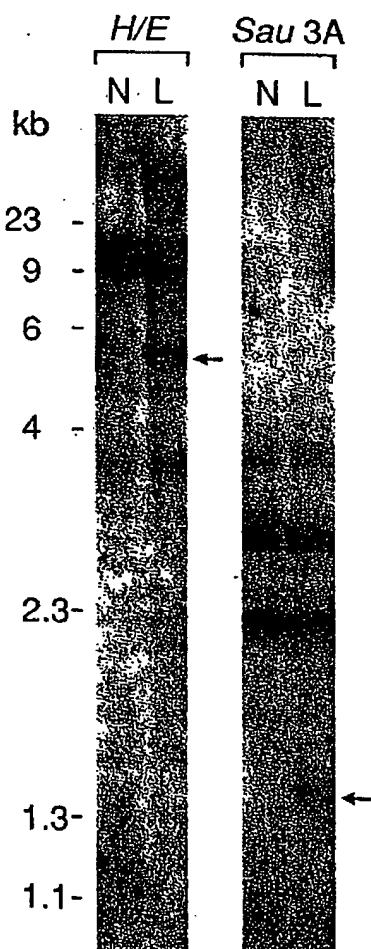


Fig 1. DNA blots of the leukemia sample. The restriction fragment pattern of normal human DNA (N) and the leukemia sample (L) were compared using a human Jh probe. Rearranged bands are indicated by arrows. Sample L exhibits a single rearranged band with both *Hind* III/*Eco*RI and *Sau*3A restriction digests. The rearranged bands are less intense than the other bands because the majority of cells in the sample represent normal bone marrow elements.

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lished methods.⁵ Approximately 100 μ g of high mol wt genomic DNA were partially digested with the *Sau*3A restriction enzyme. Fragments from 9 to 23 kilobases (kb) in size were isolated on a sucrose gradient and ligated into phage EMBL3A (Stratagene, San Diego). Recombinant phage were packaged, plated, and screened as previously reported.⁵

DNA sequencing. Fragments for sequencing were cloned into M13 vectors and sequenced by the chain termination method using Sequenase (United States Biochemical, Cleveland).⁷ All sequence data were derived from both strands.

RESULTS

We studied a bone marrow sample from a patient with ALL and associated peripheral eosinophilia. Karyotypic analysis showed the characteristic t(5;14)(q31;q32) translocation. These features define a distinctive subtype of ALL.^{3,4} The leukemic cells were analyzed for cell surface phenotype by immunofluorescence. They were positive for B1 (CD20), B4 (CD19), cALLA (CD10), HLA-DR, and terminal deoxynucleotidyl transferase (Tdt), but negative for surface immunoglobulin. This phenotypic profile describes an immature cell from the B-lymphocytic lineage.⁸

The leukemia DNA was analyzed by Southern blotting for rearrangements of the IgH gene. Using a human immunoglobulin Jh probe, a single rearranged band was detected by *Eco*RI, *Hind*III, *Sst*I, *Sau*3A, and *Eco*RI plus *Hind*III restriction digests, suggesting rearrangement of one allele (Fig 1). The immunoglobulin Jh region from the other allele was presumably either deleted or in the germline configuration.

We hypothesized that the t(5;14)(q31;q32) juxtaposed a

growth-promoting gene on chromosome 5 with the immunoglobulin Jh region on chromosome 14. Therefore, a genomic library was made from the leukemic sample and screened with a Jh probe. Fifteen distinct positive clones were isolated and screened for the presence of the rearranged *Sau*3A fragment that was detected by DNA blotting. By this analysis, five clones appeared to represent the rearranged allele identified by DNA blots. One of these clones (clone no. 4) was chosen for further study and a detailed restriction map was generated. The *Eco*RI, *Hind*III/*Eco*RI, and *Sst*I fragments from clone no. 4 that hybridized to the human Jh probe were also identical in size to the rearranged fragments from the leukemia sample, confirming that clone no. 4 represented the rearranged leukemic allele.

Phage clone no. 4 contained 3.7 kb of unknown origin joined to the IgH gene in the region of Jh4 (Fig 2). The IgH gene from Jh4 to the Cmu region appeared to be in germline configuration. Previously, the gene encoding hematopoietic growth factor IL-3 had been mapped to chromosome 5q31 so it was suspected that clone no. 4 might contain part of this gene.^{9,12} When the restriction map of human IL-3 and clone no. 4 were compared, they were identical for more than 3 kb (Fig 2).

We confirmed the juxtaposition of the IL-3 gene and the IgH gene by nucleic acid sequencing of the subcloned *Bst*EII/*Hpa*I fragment (Fig 2). The sequence of this fragment showed no disruption of the protein coding region or the messenger RNA of the IL-3 gene. The break in the IL-3 gene occurred in the promoter region, 452 base pairs (bp) upstream of the transcriptional start site (position 64, Fig

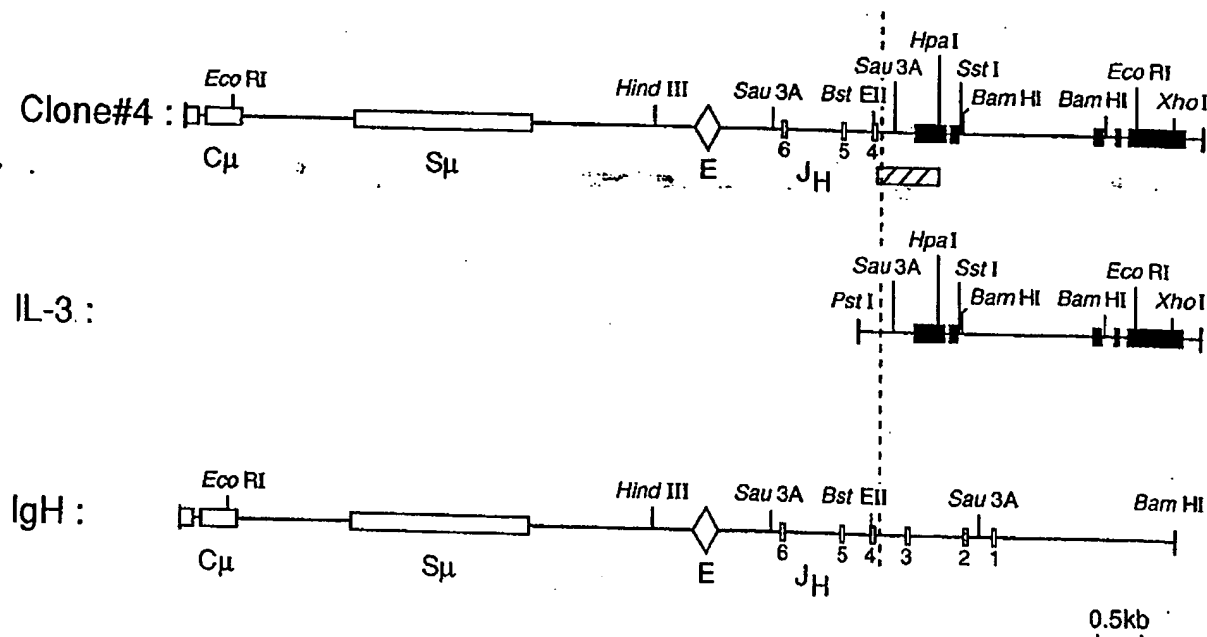


Fig 2. Breakpoint region: t(5;14)(q31;q32). Comparative mapping of phage clone no. 4, the germline IgH region, and the germline IL-3 gene.^{9,12} The map of clone no. 4 is identical to that of IgH until it diverges in the region of Jh4 (at the dashed line), after which it is identical to the map of IL-3. The two genes are positioned in a head-to-head orientation. The Ig μ chain constant region (C μ), switch region (S μ), hatched box indicates the sequenced region. The five exons (dark boxes) and four introns of the IL-3 gene are shown. The

3A). The break in the IgH gene occurred 2 bp upstream of the Jh4 region. Between the two breaks, 25 bp of uncertain origin (putative N sequence) were inserted.^{13,14} No sequences homologous to the immunoglobulin heptamer and nonamer could be identified in the IL-3 sequence (Fig 3B). Therefore, nucleic acid sequencing confirmed the juxtaposition of the IL-3 gene and the IgH gene. The sequence data clearly showed that the genes were positioned in opposite transcriptional orientations (head-to-head).

Available data also allowed us to determine the normal positions of the IL-3 gene and the GM-CSF gene in relation to the centromere of chromosome 5 (Fig 4). The IgH gene is known to be positioned with the variable regions toward the telomere on chromosome 14q.^{2,15} It has also been shown that

GM-CSF maps within 9 kb of IL-3 in the same transcriptional orientation.¹⁶ Using this information and assuming a simple translocation event in our sample, we can conclude that the IL-3 gene is normally more centromeric, and the GM-CSF gene more telomeric on chromosome 5q (Fig 4). Furthermore, both are transcribed with their 5' ends toward the centromere.

DISCUSSION

In this report we have cloned a unique chromosomal translocation that appears to be a consistent feature of a rare, yet distinct, clinical form of acute leukemia. This translocation joined the promotor of the IL-3 gene to the IgH gene. Except for the altered promotor, the IL-3 gene appeared

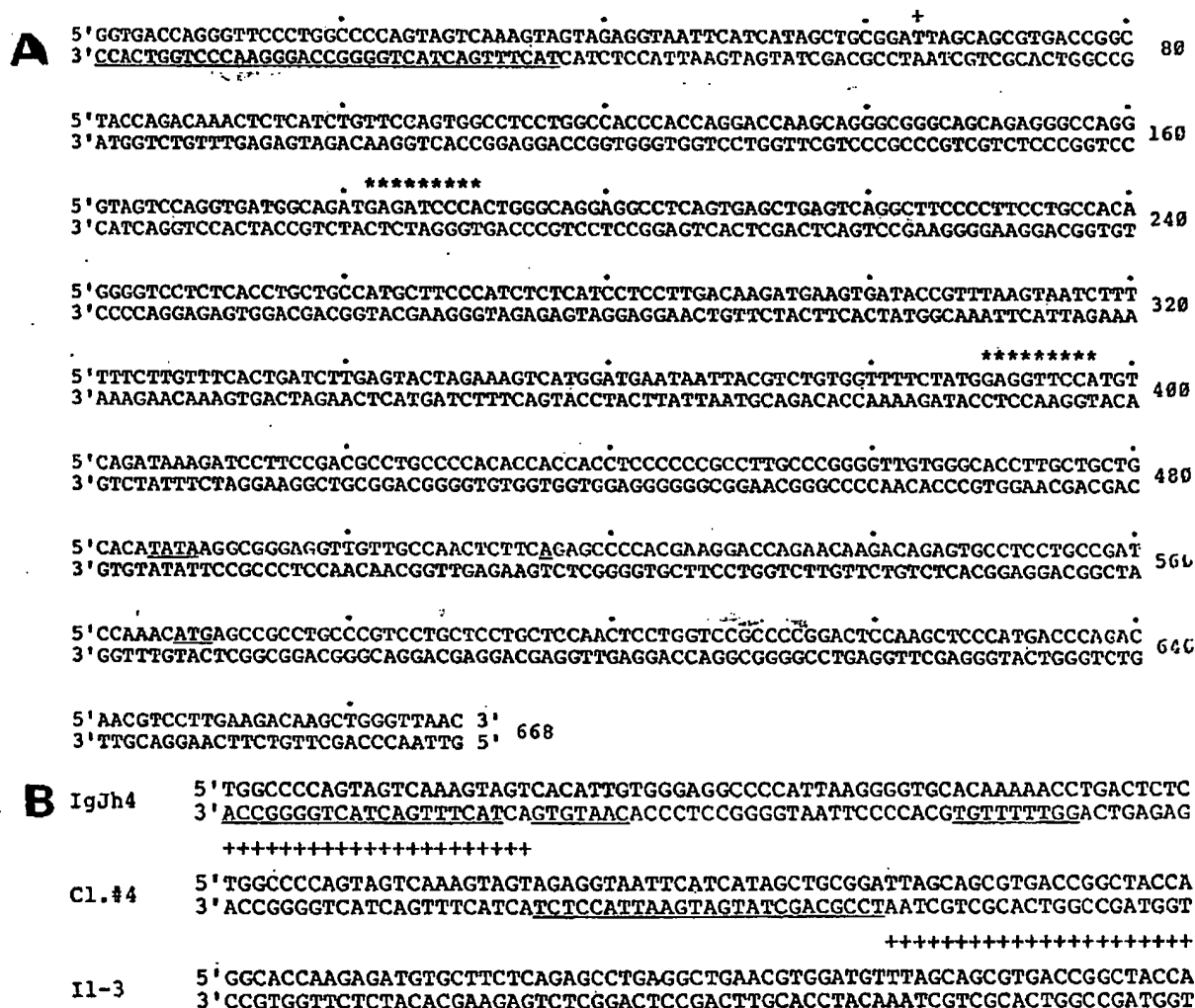


Fig 3. Sequence of t(5;14)(q31;q32) breakpoint region. (A) Nucleotide sequence of the *Bst*II/*Hpa*I fragment indicated on Fig 2. Nucleotides 1 to 36 represent the Jh4 coding region underlined on the coding strand.⁹ Nucleotides 39 to 63 are a putative N region. The sequence from position 64 to 668 is that of the germline IL-3 gene.²² The IL-3 TATA box (485), transcription start (515), and initiation methionine (567) are underlined. Two proposed regulatory sequences in the promotor are marked by asterisks (positions 182 and 389). (B) Comparative sequence of the t(5;14)(q31;q32) breakpoint region. The IgJh4 region is shown with its coding region, heptamer, and nonamer underlined. Clone no. 4 is shown with putative N region sequences underlined. The IL-3 sequence is also shown. A plus sign (+) denotes the identical nucleotide between sequences. No heptamer or nonamer is identified in the IL-3 sequence.

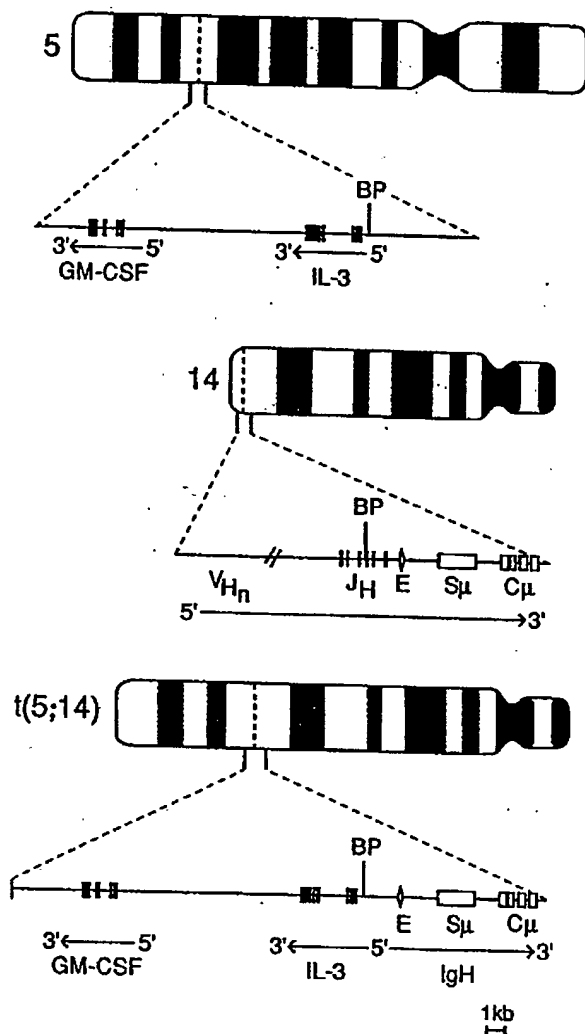


Fig 4. Diagram of the translocation. The normal chromosome 5q31 is shown with the GM-CSF gene telomeric to the IL-3 gene in the transcriptional orientation shown. On normal chromosome 14q32 the Vh regions are telomeric. The t(5;14)(q31;q32) translocation results in the head-to-head orientation of these genes. Symbols are defined in Fig 2. BP, breakpoint position.

intact as no deletions, insertions, or point mutations were detected by restriction mapping of the entire gene and sequencing of part of the gene. The IgH gene has been truncated at the Jh4 region, which places the immunoglobulin enhancer within 2.5 kb of the IL-3 gene.^{17,18} This leads to the hypothesis that the enhancer is increasing transcription of a structurally normal IL-3 gene. The same mechanism is important for activation of the *c-myc* gene in some cases of Burkitt's lymphoma.¹⁹ An alternate hypothesis is that the elimination of an upstream IL-3 promoter element is crucial to the activation of the IL-3 gene.

The proposed activation of the IL-3 gene suggests that an autocrine loop is important for the pathogenesis of this leukemia.²⁰ Over-expression of the IL-3 gene coupled with

the presence of the IL-3 receptor in these cells could account for a strong stimulus for proliferation. In this regard, there are data indicating that immature B-lineage lymphocytes and B-lineage leukemias may express the IL-3 receptor.^{21,22}

An additional feature of this type of leukemia is the dramatic eosinophilia, consisting of mature forms. It has been hypothesized that the eosinophils do not arise from the malignant clone, but are stimulated by the tumor.^{23,24} Because of the known effect of IL-3 on eosinophil differentiation, secretion of high levels of IL-3 by leukemic cells might have a role in the eosinophilia in this type of leukemia.¹²

The data suggest that the recombination mechanism that is active in the IgH gene during normal differentiation has a role in this translocation.^{13,14} This is supported by the breakpoint location at the 5' end of Jh4 and the presence of putative N-region sequences. On the other hand, no recombination signal sequence (heptamer and nonamer) was found in this region on chromosome 5, suggesting that additional factors also played a role. Further studies will elucidate the mechanism of this and other translocations.

In the leukemia we studied, it is possible that the immunoglobulin enhancer also activates the GM-CSF gene, since this gene is probably positioned only 14 kb away (Fig 4). This is known to be within the range of enhancer activation.²⁵ The interleukin-5 (IL-5) gene maps to chromosome 5q31.²⁶ Deregulation of the IL-5 gene by this translocation would act synergistically with IL-3 in the stimulation of eosinophil proliferation and differentiation.²⁷ These and other questions will be answered by the study of more patient samples. We plan to determine whether the t(5;14)(q31;q32) translocation is capable of activating multiple lymphokines simultaneously and whether they cooperate in the generation of this leukemia.

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RAPID COMMUNICATION

Activation of the Interleukin-3 Gene by Chromosome Translocation in Acute Lymphocytic Leukemia With Eosinophilia

By Timothy C. Meeker, Dan Hardy, Cheryl Willman, Thomas Hogan, and John Abrams

The t(5;14)(q31;q32) translocation from B-lineage acute lymphocytic leukemia with eosinophilia has been cloned from two leukemia samples. In both cases, this translocation joined the IgH gene and the interleukin-3 (IL-3) gene. In one patient, excess IL-3 mRNA was produced by the leukemic cells. In the second patient, serum IL-3 levels were measured and shown to correlate with disease

activity. There was no evidence of excess granulocyte/macrophage colony stimulating factor (GM-CSF) or IL-6 expression. Our data support the formulation that this subtype of leukemia may arise in part because of a chromosome translocation that activates the IL-3 gene, resulting in autocrine and paracrine growth effects.

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A NUMBER OF chromosome translocations have been associated with human leukemia and lymphoma. In many cases the study of these translocations has led to the discovery or characterization of proto-oncogenes, such as *bcl-2*, *c-abl*, and *c-myc*, that are located adjacent to the translocation.^{1,2} It is now widely understood that cancer-associated translocations disrupt nearby proto-oncogenes.

A distinct subtype of acute leukemia is characterized by the triad of B-lineage immunophenotype, eosinophilia, and the t(5;14)(q31;q32) translocation.^{3,4} Leukemic cells from such patients have been positive for terminal deoxynucleotidyl transferase (Tdt), common acute lymphoblastic leukemia antigen (CALLA), and CD19, but negative for surface or cytoplasmic immunoglobulin. In previous work, we cloned the t(5;14) breakpoint from one leukemic sample (Case 1) and determined that the IgH and interleukin-3 (IL-3) genes were joined by this abnormality.⁵ In this report, we extend those findings by showing that the t(5;14)(q31;q32) translocation from a second leukemia sample (Case 2) has a similar structure, and we report our study of growth factor expression in these patients.

MATERIALS AND METHODS

Samples and Southern blots. Case 1 has been described.^{5,6} Clinical features of Case 2 have been described in detail.⁷ DNA isolation and Southern blotting was done using previously described methods.⁸ Filters were hybridized with an immunoglobulin Jh probe, a 280 bp *Bam*HI/*Eco*RI genomic IL-3 fragment, and an IL-3 cDNA probe.^{7,8}

Northern blots. RNA isolation and Northern blotting have been described.⁹ Briefly, Northern blots were done by separating 9 µg total RNA on 1% agarose-formaldehyde gels. Equal RNA loading in each lane was confirmed by ethidium bromide staining. Blots were hybridized with an IL-3 cDNA probe extending to the *Xho*I site in exon 5, a 720 bp *Sst*I/*Kpn*I probe derived from intron 2 of the IL-3 gene, a 600 bp *Nhe*I/*Hpa*I IL-5 cDNA probe, and a 500 bp *Pst*I/*Nco*I granulocyte-macrophage colony stimulating factor (GM-CSF) cDNA probe.^{10,12}

Polymerase chain reaction. Primers were designed with *Bam*HI sites for cloning. One primer hybridized to the Jh sequences from the IgH gene (Primer 144: 5'-TAGGATCCGACGGTGACCAGGGT), and the other hybridized to the region of the TATA box in the IL-3 gene (Primer 161: 5'-AACAGGATCCCGCCTTATATGTGCAG). Polymerase chain reaction (PCR) (95°C for 1 minute, 61°C for 30 seconds, and 72°C for 3 minutes) was done using 500 ng genomic DNA and 50 pmol of each primer in 100 µL containing 67 mmol/L Tris-HCl pH 8.8, 6.7 mmol/L MgCl₂, 10% dimethyl sulfoxide (DMSO), 170 µg/mL bovine serum albumin (BSA) (fraction V),

16.6 mmol/L ammonium sulfate, 1.5 mmol/L each dNTP and Taq polymerase (Perkin-Elmer, Norwalk, CT).¹³

Sequencing. Sequencing was done by chain termination in M13 vectors.¹⁴ As part of this study, we sequenced a subclone of a normal IL-3 promoter, covering 598 base pairs from a *Sma*I site at position -1240 (with respect to the proposed site of transcription initiation) to an *Nhe*I site at position -642. The plasmid containing this region was a gift from Naoko Arai of the DNAX Research Institute.

Expression in Cos7 cells. A genomic IL-3 fragment from Case 1 was cloned into the pXM expression vector.¹⁰ Briefly, the *Hind*III/*Sal*I fragment containing the IL-3 gene was subcloned from the previously described phage clone 4 into pUC18.⁵ The 2.6 kb fragment extending from the *Sma*I site 61 bp upstream of the IL-3 transcription start to the *Sma*I site in the polylinker was cloned into the blunt *Xho*I site of pXM. The negative control construct was the pXM vector without insert. Plasmids were introduced into Cos7 cells by electroporation, and supernatant was collected after 48 hours in culture.

TF1 bioassay. TF-1 cells were passaged in RPMI 1640 supplemented with 10% heat-inactivated fetal bovine serum, 2 mmol L-glutamine, and 1 ng/mL human GM-CSF.¹⁵ Samples and antibodies were diluted in this same medium lacking GM-CSF but containing penicillin and streptomycin. A 25 µL volume of serial dilutions of patient serum was added to wells in a flat bottom 96-well microtiter plate. Rat anti-cytokine monoclonal antibody in a volume of 25 µL was added to appropriate wells and preincubated for 1 hour at 37°C. Fifty microliters of twice washed TF-1 cells were added to each well, giving a final cell concentration of 1 × 10⁴ cells per well (final volume, 100 µL). The plate was incubated for 48 hours. The remaining cell viability was determined metabolically by the colori-

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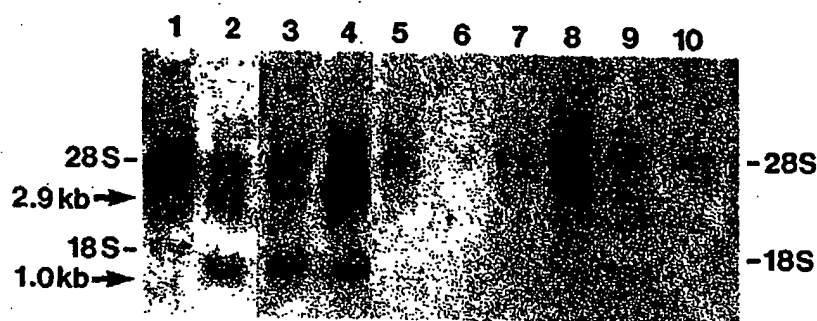


Fig 3. Documentation of IL-3 mRNA over-expression. A Northern blot was prepared and hybridized with a probe for IL-3. Lane 1 contained RNA from unstimulated peripheral blood lymphocytes (PBL) as a negative control. Lane 2 contained RNA from PBL stimulated for 4 hours with concanavalin A (ConA), and lane 3 contained RNA from PBL stimulated with ConA for 48 hours. As in the positive control lanes (2 and 3), a 1 kb band was identified in the leukemic sample from Case 1 (lane 4, lower arrow), suggesting aberrant expression of the IL-3 gene. In addition, the leukemic sample showed over-expression of an unspliced 2.9 kb IL-3 transcript (lane 4, upper arrow). We documented that this represented an unspliced precursor of the mature 1 kb transcript by showing that this band hybridized to a probe from Intron 2 of the IL-3 gene. A similar 2.9 kb band was detected in lane 2, suggesting that an IL-3 mRNA of this size is sometimes detectable in normal mitogen-stimulated cells. Lane 5 through 10 represent RNA from six samples of B-lineage acute lymphocytic leukemia without the t(5;14) translocation, indicating that only the sample with the translocation exhibited IL-3 over-expression. Case 2 could not be analyzed by Northern blot because too few cells were available for study.

the locations of the two cloned breakpoints in relation to the IL-3 gene. The two chromosome 5 breakpoints were separated by less than 500 bp.

The genomic structure in Cases 1 and 2 suggested that a normal IL-3 gene product was over-expressed as a result of the altered promoter structure. This would predict that the IL-3 gene on the translocated chromosome was capable of making IL-3 protein. This prediction was tested by expressing a genomic fragment from the translocated allele of Case 1 containing all five IL-3 exons under the control of the SV40 promoter/enhancer in the Cos7 cell line. Cell supernatants were studied in a proliferation assay using the factor dependent erythroleukemic cell line, TF-1. The supernatants derived from transfections using the vector plus insert supported TF-1 proliferation, while supernatants from transfections using the vector alone were negative in this assay (data not shown). Furthermore, the biologic activity could be blocked by an antibody to human IL-3 (BVD3-6G8). This result showed that the translocated allele retained the ability to make IL-3 mRNA and protein.

The level of expression of IL-3 mRNA in leukemic cells from Case 1 was assessed. Northern blotting showed that the mature IL-3 mRNA (approximately 1 kb) and a 2.9 kb unspliced IL-3 mRNA were excessively produced by the leukemia (Fig 3). The 2.9 kb form of the mRNA is also present at low levels in normal peripheral blood T lymphocytes after mitogen activation (Fig 3). Several B-lineage acute leukemia samples without the t(5;14) translocation had undetectable levels of IL-3 mRNA in these experiments. In addition, although genes for GM-CSF and IL-5 map close to the IL-3 gene and might have been deregulated by the translocation, no IL-5 or GM-CSF mRNA could be detected in the leukemic sample (data not shown).^{19,20}

Three serum samples from Case 2 were assayed by immunoassay for levels of IL-3, GM-CSF, and IL-5 (Table 1). Serum IL-3 could be detected and correlated with the clinical course. When the patient's leukemic cell burden was

highest, the IL-3 level was highest. No serum GM-CSF or IL-5 could be detected.

Since the IL-3 immunoassay measured only immunoreactive factor, we confirmed that biologically active IL-3 was present by using the TF-1 bioassay. This bioassay can be rendered monospecific using appropriate neutralizing monoclonal antibodies specific for IL-3, IL-5, or GM-CSF. We observed that sera from 1-16-84 and 3-14-84 contained TF-1 stimulating activity that could be blocked with anti-IL-3 MoAb (BVD3-6G8), but not with MoAbs to IL-5 (JES1-39D10) or GM-CSF (BVD2-23B6) (Fig 4; GM-CSF data not shown). The amount of neutralizable bioactivity in these two samples correlated very well with the difference in IL-3 levels obtained by immunoassay for these samples. Furthermore, the failure to block TF-1 proliferating activity with either anti-IL-5 or anti-GM-CSF was consistent with the inability to measure these factors by immunoassay and

Table 1. Peripheral Blood Counts and Growth Factor Levels at Different Times in Case 2

	Sample Date		
	11/16/83	1/16/84	3/14/84
Peripheral blood counts (cells/ μ L)			
WBC	81,800	116,500	12,300
Lymphoblasts	0	33,785	0
Eosinophils	46,626	73,080	616
Serum growth factor levels (pg/mL)			
IL-3	<444	7,995	1,051
GM-CSF	<15	<15	<15
IL-5	<50	<50	<50

Peripheral blood counts from Case 2 at three different time points with the corresponding growth factor levels quantified by immunoassay. The patient received chemotherapy between 1/16/84 and 3/14/84 to lower his leukemic burden.³ No serum samples were available for a similar analysis of Case 1.

Abbreviation: WBC, white blood cells.

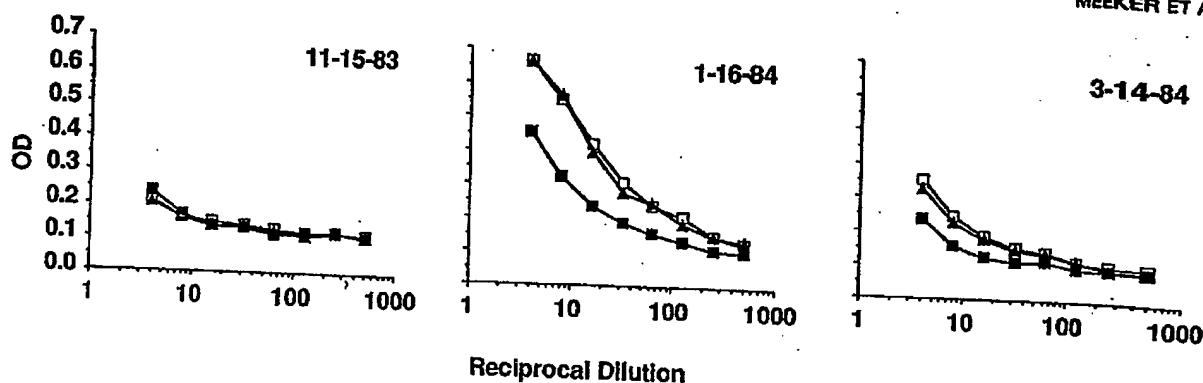


Fig 4. Bioassay of serum IL-3. Leukemic patient sera were tested for bioactive IL-3 and IL-5 in the TF-1 proliferation assay. The reciprocal of the dilution is indicated on the horizontal axis and the optical density indicating the amount of proliferation is indicated on the vertical axis. Serum from all three time points was assayed simultaneously. The assay was rendered monospecific by using a 1 μ g/mL final concentration of monoclonal rat anti-IL-3, BVD3-6G8 (■), or anti-IL-5, JES1-39D10 (▲); □ indicates no MoAb. On 1/16/84 and 3/14/84, inhibition of proliferation was evident in the presence of anti-IL-3 antibody, documenting serum levels of IL-3 on those days. Serum IL-5 was not detected in this assay, as anti-IL-5 did not alter TF-1 proliferation.

indicated that these other myeloid growth factors were not detectably circulating in the serum of this patient.

DISCUSSION

In this report, we have extended our analysis of acute lymphocytic leukemia and eosinophilia associated with the t(5;14) translocation. In both cases we have studied, we have documented the joining of the IL-3 gene from chromosome 5 to the IgH gene from chromosome 14. The breakpoints on chromosome 5 are within 500 bp of each other, suggesting that additional breakpoints will be clustered in a small region of the IL-3 promoter. The PCR assay we have developed will be useful in the screening of additional clinical samples for this abnormality.

The finding of a disrupted IL-3 promoter associated with an otherwise normal IL-3 gene implied that this translocation might lead to the over-expression of a normal IL-3 gene product. In this work, we have documented that this is true. In addition, neither GM-CSF nor IL-5 are over-expressed by the leukemic cells. Furthermore, in one patient, serum IL-3 could be measured and correlated with disease activity. To our knowledge, this is the first measurement of human IL-3 in serum and its association with a disease process. The measurement of serum IL-3 in this and other clinical settings may now be indicated.

The finding of the IL-3 gene adjacent to a cancer-associated translocation breakpoint suggests that its activation is important for oncogenesis. It is our thesis that an autocrine loop for IL-3 is important for the evolution of this leukemia.²¹ The excessive IL-3 production that we have documented would be one feature of such an autocrine loop. The final proof of our thesis must await additional data. In particular, from the study of additional clinical samples, it will be necessary to document that the IL-3 receptor is present on the leukemic cells and that anti-IL-3 antibody decreases proliferation of the leukemia in vitro.

An important aspect of this work is the suggestion of a therapeutic approach for this disease. If an autocrine loop for IL-3 can be documented in this disease, attempts to lower circulating IL-3 levels or block the interaction of IL-3 with its receptor may prove useful. Because it is also possible that the eosinophilia in these patients is mediated by the paracrine effects of leukemia-derived IL-3, similar interventions may improve this aspect of the disease. Antibodies or engineered ligands to accomplish these goals may soon be available.

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Clinical and Pathologic Significance of the *c-erbB-2* (*HER-2/neu*) Oncogene

Timothy P. Singleton and John G. Strickler

The *c-erbB-2* oncogene was first shown to have clinical significance in 1987 by Slamon et al,⁷⁹ who reported that *c-erbB-2* DNA amplification in breast carcinomas correlated with decreased survival in patients with metastasis to axillary lymph nodes. Subsequent studies, however, of *c-erbB-2* activation in breast carcinoma reached conflicting conclusions about its clinical significance. This oncogene also has been reported to have clinical and pathologic implications in other neoplasms. Our review summarizes these various studies and examines the clinical relevance of *c-erbB-2* activation, which has not been emphasized in recent reviews.^{37,38,55} The molecular biology of the *c-erbB-2* oncogene has been extensively reviewed^{37,39,55} and will be discussed only briefly here.

BACKGROUND

The *c-erbB-2* oncogene was discovered in the 1980s by three lines of investigation. The *neu* oncogene was detected as a mutated transforming gene in neuroblastomas induced by ethylnitrosurea treatment of fetal rats.^{8,73,74,78} The *c-erbB-2* was a human gene discovered by its homology to the retroviral gene *v-erbB*.^{33,49,76} *HER-2* was isolated by screening a human genomic DNA library for homology with *v-erbB*.²⁴ When the DNA sequences were determined subsequently, *c-erbB-2*, *HER-2*, and *neu* were found to represent the same gene. Recently, the *c-erbB-2* oncogene also has been referred to as *NGL*.

The *c-erbB-2* DNA is located on human chromosome 17q21^{24,33,68} and codes for *c-erbB-2* mRNA (4.6 kb), which translates *c-erbB-2* protein (p185). This

protein is a normal component of cytoplasmic membranes. The *c-erbB-2* oncogene is homologous with, but not identical to, *c-erbB-1*, which is located on chromosome 7 and codes for the epidermal growth factor receptor.^{8,103} The *c-erbB-2* protein is a receptor on cell membranes and has intracellular tyrosine kinase activity and an extracellular binding domain.^{2,105} Electron microscopy with a polyclonal antibody detects *c-erbB-2* immunoreactivity on cytoplasmic membranes of neoplasms, especially on microvilli and the non-villous outer cell membrane.⁶¹ In normal cells, immunohistochemical reactivity for *c-erbB-2* is frequently present at the basolateral membrane or the cytoplasmic membrane's brush border.^{22,52}

There is experimental evidence that *c-erbB-2* protein may be involved in the pathogenesis of breast neoplasia. Overproduction of otherwise normal *c-erbB-2* protein can transform a cell line into a malignant phenotype.²⁵ Also, when the *neu* oncogene containing an activating point mutation is placed in transgenic mice with a strong promoter for increased expression, the mice develop multiple independent mammary adenocarcinomas.^{18,63} In other experiments, monoclonal antibodies against the *neu* protein inhibit the growth (in nude mice) of a *neu*-transformed cell line,²⁶⁻²⁸ and immunization of mice with *neu* protein protects them from subsequent tumor challenge with the *neu*-transformed cell line.¹⁴ Some authors have speculated that the use of antagonists for the unknown ligand could be useful in future chemotherapy.⁶⁵ Further review of this experimental evidence is beyond the scope of this article.

The *c-erbB-2* activation most likely occurs at an early stage of neoplastic development. This hypothesis is supported by the presence of *c-erbB-2* activation in both in situ and invasive breast carcinomas. In addition, studies of metastatic breast carcinomas usually demonstrate uniform *c-erbB-2* activation at multiple sites in the same patient,^{11,12,39,41,52} although *c-erbB-2* activation has rarely been detected in metastatic lesions but not in the primary tumor.^{67,69,107} Even more rarely, *c-erbB-2* DNA amplification has been detected in a primary breast carcinoma but not in its lymph node metastasis.⁵ In patients who have bilateral breast neoplasms, both lesions have similar patterns of *c-erbB-2* activation, but only a few such cases have been studied.¹¹

MECHANISMS OF *c-erbB-2* ACTIVATION

The most common mechanism of *c-erbB-2* activation is genomic DNA amplification, which almost always results in overproduction of *c-erbB-2* mRNA and protein.^{17,34,65,81} The *c-erbB-2* amplification may stabilize the overproduction of mRNA or protein through unknown mechanisms. Human breast carcinomas with *c-erbB-2* amplification contain 2 to 40 times more *c-erbB-2* DNA^{4,5} and 4 to 128 times more *c-erbB-2* mRNA^{34,80} than found in normal tissue. Most human breast carcinomas with *c-erbB-2* amplification have 2 to 15 times more *c-erbB-2* DNA. Tumors with greater amplification tend to have greater overproduction.^{17,52,65} The non-mammary neoplasms that have been studied tend to have

similar levels of c-erbB-2 amplification or overproduction relative to the corresponding normal tissue.

The second most common mechanism of c-erbB-2 activation is overproduction of c-erbB-2 mRNA and protein without amplification of c-erbB-2 DNA.⁸¹ The quantities of mRNA and protein usually are less than those in amplified cases and may approach the small quantities present in normal breast or other tissues.^{17,50,52} The c-erbB-2 protein overproduction without mRNA overproduction or DNA amplification has been described in a few human breast carcinoma cell lines.⁴⁷

Other rare mechanisms of c-erbB-2 activation have been reported. Translocations involving the c-erbB-2 gene have been described in a few mammary and gastric carcinomas, although some reported cases may represent restriction fragment length polymorphisms or incomplete restriction enzyme digestions that mimic translocations.^{31,65,76,84,90,108} A single point mutation in the transmembrane portion of *neu* has been described in rat neuroblastomas induced by ethylnitrosurea.^{9,65} The mutated *neu* protein has increased tyrosine kinase activity and aggregates at the cell membrane.^{10,83,98} Although there has been speculation that some of the amplified c-erbB-2 genes may contain point mutations,⁴⁶ none has been detected in primary human neoplasms.^{41,53,81}

TECHNIQUES FOR DETECTING c-erbB-2 ACTIVATION

Detection of c-erbB-2 DNA Amplification

Amplification of c-erbB-2 DNA is usually detected by DNA dot blot or Southern blot hybridization. In the dot blot method, the extracted DNA is placed directly on a nylon membrane and hybridized with a c-erbB-2 DNA probe. In the Southern blot method, the extracted DNA is treated with a restriction enzyme, and the fragments are separated by electrophoresis, transferred to a nylon membrane, and hybridized with a c-erbB-2 DNA probe. In both techniques, c-erbB-2 amplification is quantified by comparing the intensity (measured by densitometry) of the hybridization bands from the sample with those from control tissue.

Several technical problems may complicate the measurement of c-erbB-2 DNA amplification. First, the extracted tumor DNA may be excessively degraded or diluted by DNA from stromal cells.⁸¹ Second, the c-erbB-2 DNA probe must be carefully chosen and labeled. For example, oligonucleotide c-erbB-2 probes may not be sensitive enough for measuring a low level of c-erbB-2 amplification, because diploid copy numbers can be difficult to detect (unpublished data). Third, the total amounts of DNA in the sample and control tissue must be compensated for, often with a probe to an unamplified gene. Many studies have used control probes to genes on chromosome 17, the location of c-erbB-2, to correct for possible alterations in chromosome number. Identical results, however, are obtained by using control probes to genes on other chromosomes,^{5,65,80} with rare exception.¹⁷ Studies using control probes to the beta-

globin gene must be interpreted with caution, because one allele of this gene is deleted occasionally in breast carcinomas.³

Amplification of *c-erbB-2* DNA was assessed by using the polymerase chain reaction (PCR) in one recent study.³² Oligoprimers for the *c-erbB-2* gene and a control gene are added to the sample's DNA, and PCR is performed. If the sample contains more copies of *c-erbB-2* DNA than of the control gene, the *c-erbB-2* DNA is replicated preferentially.

Detection of *c-erbB-2* mRNA Overproduction

Overproduction of *c-erbB-2* mRNA usually is measured by RNA dot blot or Northern blot hybridization. Both techniques require extraction of RNA but otherwise are analogous to DNA dot blot and Southern blot hybridization. Use of PCR for detection of *c-erbB-2* mRNA has been described in two recent abstracts.^{69,102}

Overproduction of *c-erbB-2* mRNA can be measured by *in situ* hybridization. Sections are mounted on glass slides, treated with protease, hybridized with a radiolabeled probe, washed, treated with nuclease to remove unbound probe, and developed for autoradiography. Silver grains are seen only over tumor cells that overproduce *c-erbB-2* mRNA. Negative control probes are used.^{65,66,106} Our experience indicates that these techniques are relatively insensitive for detecting *c-erbB-2* mRNA overproduction in routinely processed tissue. Although the sensitivity may be increased by modifications that allow simultaneous detection of *c-erbB-2* DNA and mRNA, *in situ* hybridization still is cumbersome and expensive (unpublished data).

All of the above *c-erbB-2* mRNA detection techniques have several problems that make them more difficult to perform than techniques for detecting DNA amplification. One major problem is the rapid degradation of RNA in tissue that is not immediately frozen or fixed. In addition, during the detection procedure, RNA can be degraded by RNase, a ubiquitous enzyme, which must be eliminated meticulously from laboratory solutions. Third, control probes to genes that are uniformly expressed in the tissue of interest need to be carefully selected.

Detection of *c-erbB-2* Protein Overproduction

The most accurate methods for detecting *c-erbB-2* protein overproduction are the Western blot method and immunoprecipitation. Both techniques can document the binding specificity of various antibodies against *c-erbB-2* protein. In Western blot studies, protein is extracted from the tissue, separated by electrophoresis (according to size), transferred to a membrane, and detected by using antibodies to *c-erbB-2*. In immunoprecipitation studies, antibodies against *c-erbB-2* are added to a tumor lysate, and the resulting protein-antibody precipitate is separated by gel electrophoresis and stained for protein. Both Western blot and immunoprecipitation are useful research tools but currently are not practical for diagnostic pathology. Two recent abstracts have described an enzyme-linked immunosorbent assay (ELISA) for detection of *c-erbB-2* protein.^{19,45}

Overproduction of c-erbB-2 protein is most commonly assessed by various immunohistochemical techniques. These procedures often generate conflicting results, which are explained at least partially by three factors. First, various studies have used different polyclonal and monoclonal antibodies. Because some polyclonal antibodies recognize weak bands in addition to the c-erbB-2 protein band on Western blot or immunoprecipitation, the results of these studies should be interpreted with caution.^{22,36,47,61} Even some monoclonal antibodies immunoprecipitate protein bands in addition to c-erbB-2 (p185).^{30,59,66} Second, tissue fixation contributes to variability between studies. For example, some antibodies detect c-erbB-2 protein only in frozen tissue and do not react in fixed tissue. In general, formalin fixation diminishes the sensitivity of immunohistochemical methods and decreases the number of reactive cells.^{61,66} When Bouin's fixative is used, there may be a higher percentage of positive cases.²² Third, minimal criteria for interpreting immunohistochemical staining are generally lacking. Although there is general agreement that distinct crisp cytoplasmic membrane staining is diagnostic for c-erbB-2 activation in breast carcinoma, the number of positive cells and the staining intensity required to diagnose c-erbB-2 protein overproduction varies from study to study and from antibody to antibody. Degradation of c-erbB-2 protein is not a problem because it can be detected in intact form more than 24 hours after tumor resection without fixation or freezing.⁶⁴

ACTIVATION OF c-erbB-2 IN BREAST LESIONS

Incidence of c-erbB-2 Activation

Most studies of c-erbB-2 oncogene activation do not specify histological subtypes of infiltrating breast carcinoma. Amplification of c-erbB-2 DNA was found in 19.1 percent (519 of 2715) of invasive carcinomas in 25 studies (Table 1), and c-erbB-2 mRNA or protein overproduction was detected in 20.9 percent (566 of 2714) of invasive carcinomas in 20 studies. Twelve studies have documented c-erbB-2 mRNA or protein overproduction in 15 percent (88 of 604) of carcinomas that lacked c-erbB-2 DNA amplification.

The incidence of c-erbB-2 activation in infiltrating breast carcinoma varies with the histological subtype. Approximately 22 percent (142 of 650) of infiltrating ductal carcinomas have c-erbB-2 activation, as expected from the above data. Other variants of breast carcinoma with frequent c-erbB-2 activation are inflammatory carcinoma (62 percent, 54 of 87), Paget's disease (82 percent, 9 of 11), and medullary carcinoma (22 percent, 5 of 23). In contrast, c-erbB-2 activation is infrequent in infiltrating lobular carcinoma (7 percent, 5 of 73) and tubular carcinoma (7 percent, 1 of 15).

The c-erbB-2 protein overproduction is present in 44 percent (44 of 100) of ductal carcinomas in situ and especially comedocarcinoma in situ (68 percent, 49 of 72). The micropapillary type of ductal carcinoma in situ also tends to have c-erbB-2 activation,^{40,54,68} especially if larger cells are present. The greater fre-

TABLE 1. c-erbB-2 ACTIVATION IN MALIGNANT HUMAN BREAST NEOPLASMS

Histological Diagnosis	c-erbB-2 DNA Amplification ^a	c-erbB-2 mRNA Overproduction	c-erbB-2 Protein Overproduction ^b
Carcinoma, type not specified but lacking c-erbB-2 DNA amplification	146/526, ^a 52/310, ¹⁷	42/180, ⁵⁰ 49/126, ³⁰	118/728, ^{85b}
	52/291, ¹⁰⁰ 28/176, ⁵⁷	19/62, ⁵⁵ 19/57, ⁵⁰	58/330, ^{17b} 47/313, ⁸⁶
	17/157, ¹¹³ 22/141, ³⁵	3/11, ⁵⁰ 6/10, ³⁴ 3/30 ¹	17/195, ¹¹ 32/191, ⁸⁸
	14/136, ³⁷ 12/122, ⁴		31/185, ¹⁰¹ 34/102, ⁴²
	19/103, ⁷⁹ 15/95, ⁵⁰		24/53, ^{85b} 23/47, ³³
	15/86, ¹¹¹ 17/73, ⁷⁷		22/45, ⁸ 11/36, ⁹⁴
	16/56, ⁴² 6/51, ⁵³		7/24, ⁸¹ 1/10 ⁸¹
	11/57, ⁵² 10/57, ⁵⁵		
	13/51, ¹³ 8/49, ⁵¹		
	10/36, ²² 12/36, ³⁴		
	1/25, ¹⁵ 7/24, ⁹¹		
	7/15, ³¹ 7/10, ⁹⁸		
	2/10 ¹⁰⁷		
Infiltrating ductal carcinoma	21/118, ⁵² 23/107, ³⁴	18/136, ⁸¹ 14/73, ³⁴	16/231, ^{17b} 18/136, ⁸¹
	17/50, ⁴⁴ 7/37 ⁹⁹	8/16, ⁵⁵ 0/8, ⁵⁰ 1/4, ³¹	13/35, ¹³ 14/29, ^{85b}
	14/53 (comedo-carcinoma) ¹⁸	0/3 ⁹⁸	1/28, ²² 3/24, ⁹⁴
Infiltrating ductal carcinoma	3/33 (tubuloductal carcinoma) ¹⁶	35/85 ³⁴	0/17 ⁹¹
			22/137, ⁵⁰ 14/83, ⁹⁹
			9/34 ⁸⁸

Inflammatory carcinoma	33/80, ³⁵ 3/6 ³²	46/75 ³⁵	5/6 ^{32b}
Page's disease	—	—	5/6, ⁴⁰ 2/3, ⁵⁴ 2/2 ³²
Tubular carcinoma	0/5, ¹⁹ 0/1 ³⁰	—	1/9 ⁴⁰
Medullary carcinoma	2/4, ¹⁹ 0/1 ³⁴	0/1 ³⁴	1/12, ⁴⁰ 1/3, ⁵⁸ 1/2, ⁶² 0/1 ³⁰
Mucinous carcinoma	0/1, ¹⁹ 0/1 ³⁰	—	1/2 ⁵⁸
Invasive papillary carcinoma	0/2 ³⁴	—	—
Infiltrating lobular carcinoma	1/16, ¹⁹ 0/6 ³⁴	1/5 ³⁴	2/27, ³² 0/12, ⁴⁰ 0/9, ³⁰ 1/5 ³⁴
Mammary fibrosarcoma	0/1 ³⁰	—	—
"Benign cystosarcoma"	—	1/1	0/1 ³⁰
Ductal CIS ^a with minimal invasion	3/5 ³²	—	—
Ductal CIS	0/2 ³⁴	1/2 ³⁴	33/74, ⁴⁰ 10/24 ³⁰ 20/33, ⁵⁸ 19/28, ⁶² 10/10 ⁵⁴
Ductal CIS, solid or comedo type	—	—	10/10 ⁵⁸
Ductal CIS, micropapillary type	—	—	1(focal)/14 ⁵⁴
Ductal CIS, micropapillary or cribriform type	—	—	0/16, ³² 1/9, ⁵⁸ 0/3 ⁴⁰
Ductal CIS, papillary or cribriform type	—	—	0/16 ⁴⁰
Lobular CIS	—	—	—

^aShown as number of cases with activation/number of cases studied; reference is given as a superscript.

^bThese protein studies used Western blots; the rest used immunohistochemical methods.

^cCIS = carcinoma in situ.

quency of *c-erbB-2* protein overproduction in comedocarcinoma in situ, compared with infiltrating ductal carcinoma, could be explained by the fact that many infiltrating ductal carcinomas arise from other types of intraductal carcinoma, which show *c-erbB-2* activation infrequently. Others have speculated that carcinoma in situ with *c-erbB-2* activation tends to regress or to lose *c-erbB-2* activation during progression to invasion.^{40,68,62} Infiltrating and in situ components of ductal carcinoma, however, usually are similar with respect to *c-erbB-2* activation,^{11,39} although some authors have noted more heterogeneity of the immunohistochemical staining pattern in invasive than in in situ carcinoma.^{40,42,68} Activation of *c-erbB-2* is infrequent in lobular carcinoma in situ. If lesions contain more than one histological pattern of carcinoma in situ, the *c-erbB-2* protein overproduction tends to occur in the comedocarcinoma in situ but may include other areas of carcinoma in situ.^{42,54,68} Overproduction of *c-erbB-2* protein in ductal carcinoma in situ correlates with larger cell size and a periductal lymphoid infiltrate.⁶⁸

Activation of *c-erbB-2* has not been identified in benign breast lesions, including fibrocystic disease, fibroadenomas, and radial scars (Table 2). Strong membrane immunohistochemical reactivity for *c-erbB-2* has not been described in atypical ductal hyperplasia, although weak accentuation of membrane staining has been noted infrequently.^{39,42,54} In normal breast tissue, *c-erbB-2* DNA is diploid, and *c-erbB-2* is expressed at lower levels than in activated tumors.^{34,35,65,68}

These preliminary data suggest that *c-erbB-2* activation may not be useful for resolving many of the common problems in diagnostic surgical pathology. For example, *c-erbB-2* activation is infrequent in tubular carcinoma and radial scars. In addition, because *c-erbB-2* activation is unusual in atypical ductal hyperplasia, cribriform carcinoma in situ, and papillary carcinoma in situ, detection of *c-erbB-2* activation in these lesions may not be helpful in their differential diagnosis. The histological features of comedocarcinoma in situ, which commonly overproduces *c-erbB-2*, are unlikely to be mistaken for those of benign lesions. Activation of

TABLE 2. *c-erbB-2* ACTIVATION IN BENIGN HUMAN BREAST LESIONS

Histological Diagnosis	<i>c-erbB-2</i> DNA Amplification ^a	<i>c-erbB-2</i> mRNA Overproduction	<i>c-erbB-2</i> Protein Overproduction
Fibrocystic disease	0/10 ³³	—	0/32, ³⁹ 0/9, ⁶⁸ 0/8 ⁶⁵
Atypical ductal hyperplasia	—	—	2(weak)/21, ⁵⁴ 1(cytoplasmic)/13 ³⁹
Benign ductal hyperplasia	—	—	0/12 ³⁹
Sclerosing adenosis	—	—	0/4 ³⁹
Fibroadenomas	0/16, ³⁴ 0/6, ⁶³ 0/2, ²¹ 0/1 ³¹	0/6, ³⁵ 0/3 ³⁴	0/21, ³⁸ 0/10, ⁶⁸ 0/8, ³⁸ 0/3 ⁴²
Radial scars	—	—	0/22 ³⁵
Blunt duct adenosis	—	—	0/14 ³⁸
"Breast mastosis"	—	0/3 ³⁵	—

^aShown as number of cases with activation/number of cases studied; reference is given as a superscript.

c-erbB-2, however, does favor infiltrating ductal carcinoma over infiltrating lobular carcinoma. Further studies of these issues would be useful.

Correlation of c-erbB-2 Activation With Pathologic Prognostic Factors

Multiple studies have attempted to correlate c-erbB-2 activation with various pathologic prognostic factors (Table 3). Activation of c-erbB-2 was correlated with lymph node metastasis in 8 of 28 series, with higher histological grade in 6 of 17 series, and with higher stage in 4 of 14 series. Large tumor size was not associated with c-erbB-2 activation in most studies (11 of 14). Tetraploid DNA content and low proliferation, measured by Ki-67, have been suggested as prognostic factors and may correlate with c-erbB-2 activation.^{6,7}

Correlation of c-erbB-2 Activation With Clinical Prognostic Factors

Various studies have attempted also to correlate c-erbB-2 activation with clinical features that may predict a poor outcome (Table 4). Activation of c-erbB-2 correlated with absence of estrogen receptors in 10 of 28 series and with absence of progesterone receptors in 6 of 18 series. In most studies, patient age did not correlate with c-erbB-2 activation, and, in the rest of the reports, c-erbB-2 activation was associated with either younger or older ages.

Correlation of c-erbB-2 Activation With Patient Outcome

Slamon et al^{79,81} first showed that amplification of the c-erbB-2 oncogene independently predicts decreased survival of patients with breast carcinoma. The correlation of c-erbB-2 amplification with poor outcome was nearly as strong as the correlation of number of involved lymph nodes with poor outcome. Slamon et al also reported that c-erbB-2 amplification is an important prognostic indicator only in patients with lymph node metastasis.^{79,81}

A large number of subsequent studies also attempted to correlate c-erbB-2 activation with prognosis (Table 5). In 12 series, there was a correlation between c-erbB-2 activation and tumor recurrence or decreased survival. In five of these series, the predictive value of c-erbB-2 activation was reported to be independent of other prognostic factors. In contrast, 18 series did not confirm the correlation of c-erbB-2 activation with recurrence or survival. Four possible explanations for this controversy are discussed below.

One problem is that c-erbB-2 amplification correlates with prognosis mainly in patients with lymph node metastasis. As summarized in Table 5, most studies of patients with axillary lymph node metastasis showed a correlation of c-erbB-2 activation with poor outcome. In contrast, most studies of patients without axillary metastasis have not demonstrated a correlation with patient outcome. Table 6 summarizes the studies in which all patients (with and without axillary metastasis) were considered as one group. There is a trend for studies with a higher percentage of metastatic cases to show an association between c-erbB-2 activation and poor outcome. Thus, most of the current evidence suggests that c-erbB-2 activation has prognostic value only in patients with metastasis to lymph nodes.

TABLE 3. CORRELATION OF c-erbB-2 ACTIVATION WITH PATHOLOGIC PROGNOSTIC FACTORS IN BREAST CARCINOMA

Prognostic Factor	P ^a	c-erbB-2 DNA Amplification ^b	c-erbB-2 mRNA Overproduction	c-erbB-2 Protein Overproduction ^c
Metastasis to axillary lymph nodes	<0.05 0.05-0.15 >0.15	(118) ³⁵ (105) ³⁴ (49) ²¹ (103) ⁷⁸ (86) ⁷⁸ (58) ¹¹¹ (279) ¹⁷ (176) ⁸⁷ (157) ¹¹³ (122) ⁴ (85) ⁸⁰ (50) ⁸² (50) ⁴⁴ (47) ¹³ (41) ⁸⁰	(104) ³⁵ (92) ³⁴ (9) ³¹ (50) ³⁰ — — —	(350) ⁸⁰ (36) ¹³ (189) ⁸² (329) ⁷⁸ (261) ⁸⁴ (185) ¹¹ (185) ¹⁰¹ (102) ⁸⁸ (50) ⁸⁰ (330) ⁷⁸ (189) ⁸² (350) ⁸⁰ (185) ¹⁰¹ (34) ⁸² (348) ⁷⁸ (102) ³⁰ (56) ⁸⁰
Larger size	<0.05 0.05-0.15 >0.15	(280) ¹⁷ (86) ⁷⁸ (176) ⁸⁷ (157) ¹¹³ (103) ⁷⁸ (64) ⁷⁷ (58) ¹¹¹ (45) ⁸¹ (300) ¹⁷ (64) ⁷⁷ (58) ¹¹¹ (56) ⁸² (176) ⁸⁷ (157) ¹¹³ (84) ⁸⁰ (61) ⁸⁰ (53) ⁸¹ (52) ⁸⁷ (41) ⁸⁰	(51) ⁸⁰ — — — — — —	(178) ¹⁰¹ (168) ¹¹ (38) ¹³ (280) ⁸⁰ (189) ⁸² (102) ³⁰
Higher stage	<0.05 0.05-0.15 >0.15	(47) ¹³ (15) ³¹ (122) ⁴ (113) ³⁴ (95) ⁸⁰ (58) ¹¹¹ (50) ⁴⁴ (41) ⁸⁰	(53) ⁸⁰ (86) ⁸⁰ (65) ⁸⁵ —	(178) ¹⁰¹ (168) ¹¹ (38) ¹³ (280) ⁸⁰ (189) ⁸² (102) ³⁰

^aA correlation is statistically significant at <0.05, equivocal at best between 0.05 and 0.15, and not statistically significant at >0.15.^bNumbers inside parentheses are the number of patients in an individual study; superscript is the reference. Some studies analyzed more than one group of patients.^cBy Western blot method; all other protein studies used immunohistochemical methods.

TABLE 4. CORRELATION OF c-erbB-2 ACTIVATION WITH CLINICAL PROGNOSTIC FACTORS IN BREAST CARCINOMA

Prognostic Factor	P ^a	c-erbB-2 DNA Amplification ^b	c-erbB-2 mRNA Overproduction	c-erbB-2 Protein Overproduction ^c
Absence of estrogen receptors	<0.05	(253) ¹⁰⁰ (141) ³⁵ (109) ³⁴ (86) ⁷² (50) ⁴⁴ (47) ¹³	(104) ³⁵	(350) ³⁵⁰ (330) ¹⁷⁰ (185) ¹⁰¹
	0.05-0.15	—	—	—
	>0.15	(157) ¹¹² (122) ⁴ (103) ⁷² (95) ⁹⁰ (64) ⁷⁷ (61) ⁹⁰ (58) ¹¹¹ (53) ²¹ (51) ³² (41) ⁹³	(180) ⁹⁵ (62) ⁶⁵ (62) ³⁵ (57) ⁵⁰	(230) ¹⁰⁰ (172) ¹¹ (51) ³² (38) ⁷²
Absence of progesterone receptors	<0.05	(253) ¹⁰⁰ (141) ³⁵ (109) ³⁴ (50) ⁴⁴	—	(350) ³⁵⁰ (306) ¹⁷⁰
	0.05-0.15	(86) ⁷² (49) ³²	—	—
	>0.15	(157) ¹¹² (122) ⁴ (103) ⁷² (64) ⁷⁷	(180) ⁹⁵ (103) ³⁵ (62) ³⁵ (56) ³⁵	(90) ¹¹ (49) ³²
Age (menopausal status)	<0.05	—	— ⁷⁷	(younger: 330) ¹⁷⁰ (older: 58) ³⁵⁰
	0.05-0.15	(younger: 86) ⁷² (230) ¹¹ (176) ³⁷ (157) ¹¹² (122) ⁴ (116) ³⁴ (103) ⁷²	(82) ³⁵	(350) ³⁵⁰ (290) ³⁵ (189) ³² (162) ¹¹ (45) ³²
	>0.15	(95) ⁹⁰ (64) ⁷⁷ (58) ¹¹¹ (56) ³⁵ (53) ²¹ (49) ³² (41) ⁹³ (15) ³¹	—	—

^aA correlation is statistically significant at <0.05, equivocal at best between 0.05 and 0.15, and not statistically significant at >0.15^bNumbers inside parentheses are the number of patients in an individual study; superscript is the reference. Some studies analyzed more than one group of patients.^cq; Western blot method; all other protein studies used immunohistochemical methods.

TABLE 5. CORRELATION OF c-erbB-2 ACTIVATION WITH OUTCOME IN PATIENTS WITH BREAST CARCINOMA

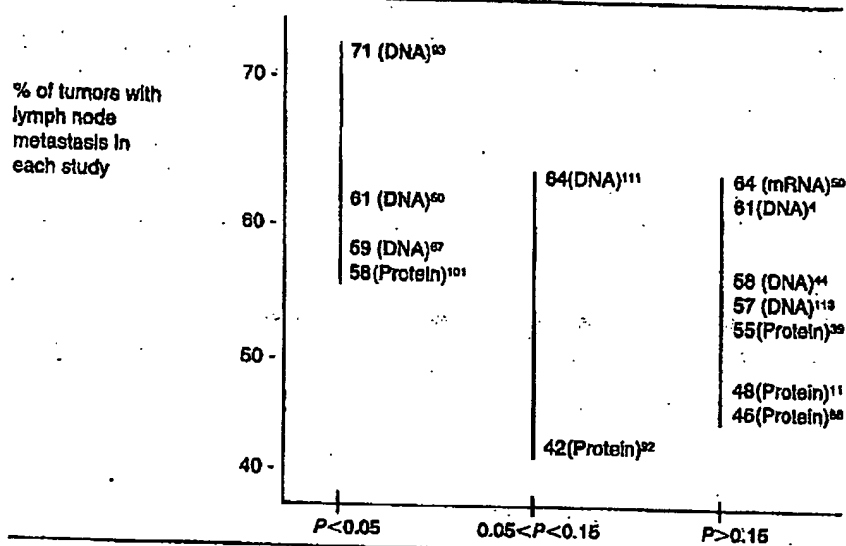
P ^a	Type of c-erbB-2 Activation ^b	Number of Patients		Statistical Analysis ^c	Reference
		Total	With Metastasis to Axillary Lymph Nodes		
<0.05	DNA	176		M	87
<0.05	DNA	61		U	60
<0.05	DNA	57		U	65
<0.05	DNA	41		U	93
<0.05	mRNA	62		U	65
<0.05	Protein	102		M	101
<0.05	DNA		345	M	81
<0.05	DNA		120	U	17
<0.05	DNA		91	U	87
<0.05	DNA		88	M	79
<0.05	Protein-WB		350	M	85
<0.05	Protein		62	U	101
0.05-0.15	DNA	57		U	111
0.05-0.15	Protein	189		M	92
0.05-0.15	Protein		120	U	86
>0.15	DNA	130		U	113
>0.15	DNA	122		M	4
>0.15	DNA	50		U	44
>0.15	mRNA	57		U	50
>0.15	Protein	290		M	88
>0.15	Protein	195		U	11
>0.15	Protein	102		U	39
>0.15	Protein		137	U	17
>0.15	DNA			M	81
>0.15	DNA			U	17
>0.15	DNA			U	87
>0.15	Protein-WB			U	85
>0.15	Protein-WB			U	17
>0.15	Protein			U	86
>0.15	Protein			U	40

^aThe endpoints of these studies were tumor recurrence or decreased survival or both. Correlation between c-erbB-2 activation and a poorer patient outcome is statistically significant at <0.05, is of equivocal significance at 0.05 to 0.15, and is not significant at >0.15.

^bShown as variable measured. Letters "WB" indicate assay by Western blot; the other protein studies used immunohistochemical methods.

^cM = multivariate statistical analysis; U = univariate statistical analysis.

TABLE 6. PERCENTAGE OF BREAST CARCINOMAS WITH METASTASIS COMPARED WITH PROGNOSTIC SIGNIFICANCE OF c-erbB-2 ACTIVATION



P for correlation of c-erbB-2 activation with patient outcome.

Each study's percentage of breast carcinomas with metastasis is compared with the correlation between c-erbB-2 activation and outcome. These data include only those studies that considered, as one group, all breast cancer patients, whether or not they had axillary metastasis. Superscripts are the references. In parentheses are the types of c-erbB-2 activation. P values are interpreted as in Table 3.

A second problem is that various types of breast carcinoma are grouped together in many survival studies. Because the current literature suggests that c-erbB-2 activation is infrequent in lobular carcinoma, studies that combine infiltrating ductal and lobular carcinomas may dilute the prognostic effect of c-erbB-2 activation in ductal tumors. In addition, most studies do not analyze inflammatory breast carcinoma separately. This condition frequently shows c-erbB-2 activation and has a worse prognosis than the usual mammary carcinoma, but it is an uncommon lesion.

A third potential problem is the paucity of studies that attempt to correlate c-erbB-2 activation with clinical outcome in subsets of breast carcinoma without metastasis. Two recent abstracts reported that in patients without lymph node metastasis who had various risk factors for recurrence (such as large tumor size and absence of estrogen receptors), c-erbB-2 overexpression predicted early recurrence.^{23,67} In patients with ductal carcinoma in situ, one small study found no association between tumor recurrence and c-erbB-2 activation.⁴⁰

A fourth problem is the lack of data regarding whether the prognosis correlates better with c-erbB-2 DNA amplification or with mRNA or protein overproduction. Most studies that find a correlation between c-erbB-2 activa-

tion and poor patient outcome measure *c-erbB-2* DNA amplification (Table 5), and breast carcinoma patients with greater amplification of *c-erbB-2* may have poorer survival.^{79,81} Recent studies suggest that amplification has more prognostic power than overproduction,^{17,34,35} but the clinical significance of *c-erbB-2* overproduction without DNA amplification deserves further research.^{17,52} Few studies have attempted to correlate patient outcome with *c-erbB-2* mRNA overproduction, and many studies of *c-erbB-2* protein overproduction use relatively less reliable methods such as immunohistochemical studies with polyclonal antibodies.

Comparison of *c-erbB-2* Activation With Other Oncogenes in Breast Carcinoma

Other oncogenes that may have prognostic implications in human breast cancer are reviewed elsewhere.^{71,106} This section will be restricted to a comparison between the clinical relevance of *c-erbB-2* and these other oncogenes.

The *c-myc* gene is often activated in breast carcinomas, but *c-myc* activation generally has less prognostic importance than *c-erbB-2* activation.^{21,34,77,87,93} One study found a correlation between increased mRNAs of *c-erbB-2* and *c-myc*, although other reports have not confirmed this.^{34,106} Subsequent research, however, could demonstrate a subset of breast carcinomas in which *c-myc* has more prognostic importance than *c-erbB-2*.

The gene *c-erbB-1* for the epidermal growth factor receptor (EGFR) is homologous with *c-erbB-2* but is infrequently amplified in breast carcinomas.⁷⁹ Overproduction of EGFR, however, occurs more frequently than amplification and may correlate with a poor prognosis. In studies that have examined both *c-erbB-2* and EGFR in the same tumor, *c-erbB-2* has a stronger correlation with poor prognostic factors.^{35,52} Studies have tended to show no correlation between amplification of *c-erbB-2* and *c-erbB-1* or overproduction of *c-erbB-2* and EGFR, although at the molecular level EGFR mediates phosphorylation of *c-erbB-2* protein.^{51,52,61,68,109} Recent reviews describe EGFR in breast carcinoma.^{43,100}

The genes *c-erbA* and *ear-1* are homologous to the thyroid hormone receptor, and they are located adjacent to *c-erbB-2* on chromosome 17. These genes are frequently coamplified with *c-erbB-2* in breast carcinomas. The absence of *c-erbA* expression in breast carcinomas, however, is evidence against an important role for this gene in breast neoplasia.⁹⁰ Amplification of *c-erbB-2* can occur without *ear-1* amplification, and these tumors have a decreased survival that is similar to tumors with both *c-erbB-2* and *ear-1* amplification.⁶⁷ Consequently, *c-erbB-2* amplification seems to be more important than amplification of *c-erbA* or *ear-1*.

Other genes also have been compared with *c-erbB-2* activation in breast carcinomas. One study found a significant correlation between increased *c-erbB-2* mRNA and increased mRNAs of *fos*, platelet-derived growth factor chain A, and *Ki-ras*.¹⁰⁶ Allelic deletion of *c-Ha-ras* may indicate a poorer prognosis in breast carcinoma,²¹ but it has not been compared with *c-erbB-2* activation. Some studies have suggested a correlation between advanced stage or recurrence of breast carcinoma and activation of any one of several oncogenes.^{21,113}

ACTIVATION OF c-erbB-2 IN NON-MAMMARY TISSUES

Incidence of c-erbB-2 Activation in Non-Mammary Tissues

Table 7 summarizes the normal tissues in which c-erbB-2 expression has been detected, usually with immunohistochemical methods using polyclonal anti-

TABLE 7. PRESENCE OR ABSENCE OF c-erbB-2 mRNA OR c-erbB-2 PROTEIN IN NORMAL HUMAN TISSUES

Tissues With c-erbB-2 mRNA	Tissues Producing c-erbB-2 Protein ^a	Tissues Lacking c-erbB-2 mRNA	Tissues Lacking c-erbB-2 Protein
Skin ²⁴	Epidermis ⁵⁰ External root sheath ⁵⁰ Eccrine sweat gland ⁵⁰ Fetal oral mucosa ⁶² Fetal esophagus ⁶²		Postnatal oral mucosa ⁶² Postnatal esophagus ⁶²
Stomach ²⁴	Stomach ^{22,62} Fetal intestine ^{62a}		
Jejunum ²⁴	Small intestine ^{22,62}		
Colon ²⁴	Colon ^{22,62}		
Kidney ²⁴	Fetal kidney ^{62a}	Kidneys ¹⁰⁴	Glomerulus ⁶² Postnatal Bowman's capsule ⁶² Postnatal proximal tubule ⁶²
	Fetal proximal tubule ⁶² Distal tubule ⁶² Fetal collecting duct ⁶² Fetal renal pelvis ⁶² Fetal ureter ⁶²		Postnatal collecting duct ⁶² Postnatal renal pelvis ⁶² Postnatal fetal ureter ⁶²
Liver ²⁴	Hepatocytes ²² Pancreatic acini ²² Pancreatic ducts ^{22,62} Endocrine cells of islets of Langerhans ²²		Liver ^{62,65} Pancreatic islets ⁶²
Lung ²⁴	Fetal trachea ⁶² Fetal bronchioles ⁶² Bronchioles ⁶²		Postnatal trachea ⁶² Postnatal bronchioles ⁶²
Fetal brain ²⁴			Postnatal alveoli ^{62,69} Postnatal brain ⁶² Postnatal ganglion cells ⁶²
Thyroid ¹	Fetal ganglion cells ⁶²		
Uterus ²⁴			
	Ovary ¹² Blood vessels ⁴²		Endothelium ⁶²
Placenta ²⁴			Adrenocortical cells ⁶² Postnatal thymus ⁶² Fibroblasts ⁶² Smooth muscle cells ⁶² Cardiac muscle cells ⁶²

^aThis protein study used Western blots; the rest used immunohistochemical methods.

bodies. Only a few studies have been performed, and some of these do not demonstrate convincing cell membrane reactivity in the published photographs. The interpretations in these studies, however, are listed, with the caveat that these findings should be confirmed by immunoprecipitation or Western or RNA blots. Production of *c-erbB-2* has been identified in normal epithelium of the gastrointestinal tract and skin. Discrepancies regarding *c-erbB-2* protein in other tissues could be due, at least in part, to differences in techniques.

The data on *c-erbB-2* activation in various non-mammary neoplasms should be interpreted with caution, because only small numbers of tumors have been studied, usually by immunohistochemical methods using polyclonal antibodies. Studies using cell lines have been excluded, because cell culture can induce amplification and overexpression of other genes, although this has not been documented for *c-erbB-2*.

Activation of *c-erbB-2* has been identified in 32 percent (64 of 203) of ovarian carcinomas in eight studies (Table 8). One abstract⁴⁵ stated that ovarian carcinomas contained significantly more *c-erbB-2* protein than ovarian non-epithelial malignancies. Another report⁶¹ showed that 12 percent of ovarian carcinomas had *c-erbB-2* overproduction without amplification.

Activation of *c-erbB-2* has been identified in 20 percent (40 of 198) of gastric adenocarcinomas in seven studies, including 33 percent (21 of 64) of

TABLE 8. *c-erbB-2* ACTIVATION IN HUMAN GYNECOLOGIC TUMORS*

Tumor Type	<i>c-erbB-2</i> DNA Amplification	<i>c-erbB-2</i> mRNA Over-production	<i>c-erbB-2</i> Protein Over-production
Ovary—carcinoma, not otherwise specified	31/120, ⁵¹ 1/11, ⁵⁷ 0/5, ¹⁰⁷ 0/5, ⁸⁴ 0/3, ¹¹² 0/2, ⁷² 0/1 ¹¹⁰	23/67 ⁶¹	23/73, ¹² 36/72 ⁶¹
Ovary—serous (papillary) carcinoma	2/7, ¹¹⁰ 1/7, ¹¹² 0/6 ⁷²	—	—
Ovary—endometrioid carcinoma	0/3 ¹¹⁰	—	—
Ovary—mucinous carcinoma	1/2, ¹¹⁰ 0/1 ⁷²	—	—
Ovary—clear cell carcinoma	0/2, ¹¹² 0/1 ⁷²	—	—
Ovary—mixed epithelial carcinoma	0/2 ⁷²	—	—
Ovary—endometrioid borderline tumor	0/1 ⁷²	—	—
Ovary—mucinous borderline tumor	0/3 ⁷²	—	—
Ovary—serous cystadenoma	0/4 ⁷²	—	—
Ovary—mucinous cystadenoma	0/2 ⁷²	—	—
Ovary—sclerosing stromal tumor	0/1 ⁷²	—	—
Ovary—fibrothecoma	0/1 ⁷²	—	—
Uterus—endometrial adenocarcinoma	0/4, ⁸⁴ 0/1 ¹¹⁰	—	—

*Shown as number of cases with amplification (or overproduction)/total number of cases studied; reference is given as superscript. All protein studies used immunohistochemical methods.

intestinal or tubular subtypes and 9 percent (4 of 47) of diffuse or signet ring cell subtypes (Table 9). Activation of c-erbB-2 has been detected in 2 percent (6 of 281) of colorectal carcinomas, although an additional immunohistochemical study detected c-erbB-2 protein in seven of eight tissues fixed in Bouin's solution. One study found greater immunohistochemical reactivity for c-erbB-2 protein in colonic adenomatous polyps than in the adjacent normal epithelium, using Bouin's fixative. Lesions with anaplastic features and progression to invasive carcinoma tended to show decreased immunohistochemical reactivity for c-erbB-2 protein.²³ Hepatocellular carcinomas (12 of 14 cases) and cholangiocarcinomas (46 of 63 cases) reacted with antibodies against c-erbB-2 in one study, but some of these "positive" cases showed only diffuse cytoplasmic staining, which

TABLE 9. c-erbB-2 ACTIVATION IN HUMAN GASTROINTESTINAL TUMORS*

Tumor Type	c-erbB-2 DNA Amplification	c-erbB-2 Protein Overproduction
Esophagus—squamous cell carcinoma	0/1 ¹⁰⁷	0/1 ⁸¹
Stomach—carcinoma, poorly differentiated	0/22 ¹⁰⁸	—
Stomach—adenocarcinoma	2/24, ⁸⁴ 2/9, ¹⁰⁷ 2/8, ¹¹¹ 2/8, ⁸⁷ 0/1 ¹⁰⁸	4/27, ²⁹ 3/10 ⁸¹
Stomach—carcinoma, intestinal or tubular type	5/10 ¹⁰⁸	16/54 ²⁹
Stomach—carcinoma, diffuse or signet ring cell type	0/2 ¹⁰⁸	4/45 ²⁹
Colorectum—carcinoma	2/49, ⁸⁴ 1/45, ¹¹¹ 1/45, ⁸⁷ 1/45, ⁸⁰ 0/40, ⁸¹ 0/32, ¹⁰⁷ 0/3 ⁸²	1/22, ²⁸ 7/8 ^{22b}
Colon—villous adenoma	0/1 ⁸⁰	—
Colon—tubulovillous adenoma	0/5 ⁸⁰	—
Colon—tubular adenoma	0/7 ⁸⁰	19/19 ^{22b}
Colon—hyperplastic polyp	0/1 ⁸⁰	—
Intestine—leiomyosarcoma	—	0/1 ⁸¹
Hepatocellular carcinoma	0/12 ¹¹¹	12/14, ²⁸ 0/2 ⁸¹
Hepatoblastoma	0/1 ⁸⁷	—
Cholangiocarcinoma	—	46/63 ²⁸
Pancreas—adenocarcinoma	—	2/80, ^{41c} 0/2 ⁴¹
Pancreas—acinar carcinoma	—	0/1 ⁴¹
Pancreas—clear cell carcinoma	—	0/2 ⁴¹
Pancreas—large cell carcinoma	—	0/3 ⁴¹
Pancreas—signet ring carcinoma	—	0/1 ⁴¹
Pancreas—chronic inflammation	—	0/14 ^{41c}

*Shown as number of cases with amplification (or overproduction)/total number of cases studied; reference is given as superscript. All protein studies used immunohistochemical methods. No studies analyzed for c-erbB-2 mRNA.

^bTissues fixed in Bouin's solution.

^cOnly cases with distinct membrane staining are interpreted as showing c-erbB-2 overproduction.

TABLE 10. *c-erbB-2* ACTIVATION IN HUMAN PULMONARY TUMORS^a

Tumor Type	<i>c-erbB-2</i> DNA Amplification	<i>c-erbB-2</i> Protein Overproduction
Non-small cell carcinoma	2/60, ⁷⁵ 0/60 ⁸¹	1/84 ⁵⁹
Epidermoid carcinoma	0/13, ⁸² 0/10, ⁸⁷ 0/6 ²⁰	3/6 ⁸⁸
Adenocarcinoma	0/21, ⁸² 1/13, ⁸³ 0/7, ¹¹¹ 0/7, ⁸⁷ 0/3 ¹⁰⁷	4/12 ⁸⁸
Large cell carcinoma	0/9, ⁸² 0/6 ²⁰	—
Small cell carcinoma	—	0/26, ⁵⁸ 0/3 ⁸⁹
Carcinoid tumor	0/1 ⁸²	0/3 ⁸⁹

^aShown as number of cases with amplification (or overproduction)/total number of cases studied; reference is given as superscript. All protein studies used immunohistochemical methods. No studies analyzed for *c-erbB-2* mRNA.

does not indicate *c-erbB-2* activation in breast neoplasms.⁸⁵ Also, some pancreatic carcinomas and chronic pancreatitis tissue had cytoplasmic immunohistochemical reactivity for *c-erbB-2* protein, in addition to the rare case of pancreatic adenocarcinoma with distinct cell membrane staining.⁴¹

Tables 10 through 14 summarize the studies of *c-erbB-2* activation in other neoplasms. The *c-erbB-2* oncogene is not activated in most of these tumors. Activation of *c-erbB-2* has been detected in 1 percent (4 of 299) of pulmonary non-small cell carcinomas in nine studies, although one additional report⁸⁰ found *c-erbB-2* protein overproduction in 41 percent (7 of 17). Renal cell carcinoma had *c-erbB-2* activation in 7 percent (2 of 30) in four studies. Overproduction of *c-erbB-2* protein was described in one transitional cell carcinoma of the urinary bladder, a grade 2 papillary lesion.⁵⁸ Squamous cell carcinoma and basal cell carcinoma of the skin may contain *c-erbB-2* protein, but it is not clear

TABLE 11. *c-erbB-2* ACTIVATION IN HUMAN HEMATOLOGIC PROLIFERATIONS^a

Tumor Type	<i>c-erbB-2</i> DNA Amplification	<i>c-erbB-2</i> mRNA Overproduction	<i>c-erbB-2</i> Protein Overproduction
Hematologic malignancies	0/23 ¹¹¹	—	—
Malignant lymphoma	0/9, ⁵⁷ 0/3 ¹⁰⁷	0/1 ¹	0/15 ⁸¹
Acute leukemia	0/14 ⁸⁷	—	—
Acute lymphoblastic leukemia	0/1 ¹⁰⁷	—	—
Acute myeloblastic leukemia	0/3 ¹⁰⁷	—	—
Chronic leukemia	0/19 ⁵⁷	—	—
Chronic lymphocytic leukemia	0/6 ¹⁰⁷	—	—
Chronic myelogenous leukemia	0/8 ¹⁰⁷	—	—
Myeloproliferative disorder	0/1 ⁵⁷	—	—

^aShown as number of cases with amplification (or overproduction)/total number of cases studied; reference is given as superscript. All protein studies used immunohistochemical methods.

TABLE 12. c-erbB-2 ACTIVATION IN HUMAN TUMORS OF SOFT TISSUE AND BONE*

Tumor Type	c-erbB-2 DNA Amplification
Sarcoma	0/10, ¹¹¹ 0/8 ⁵⁷
Malignant fibrous histiocytoma	0/1 ¹⁰⁷
Liposarcoma	0/3 ¹⁰⁷
Pleomorphic sarcoma	0/1 ¹⁰⁷
Rhabdomyosarcoma	0/1 ¹⁰⁷
Osteogenic sarcoma	0/2, ¹⁰⁷ 0/2 ⁵⁷
Chondrosarcoma	0/1 ¹⁰⁷
Ewing's sarcoma	0/1 ⁵⁷
Schwannoma	0/1 ⁵⁷

*Shown as number of cases with amplification (or overproduction)/total number of cases studied; reference is given as superscript. No studies analyzed for c-erbB-2 mRNA or c-erbB-2 protein.

whether the protein level is increased over that of normal skin.⁵⁶ Thyroid carcinomas and adenomas can have low levels of increased c-erbB-2 mRNA. One abstract described low-level c-erbB-2 DNA amplification in one of ten salivary gland pleomorphic adenomas.⁴⁹

Correlation of c-erbB-2 Activation With Patient Outcome

Very few studies have attempted to correlate c-erbB-2 activation in non-mammary tumors with outcome. Slamon et al⁸¹ showed that c-erbB-2 amplification or overexpression in ovarian carcinomas correlates with decreased survival, especially when marked activation is present. However, they did not report the stage, histological grade, or histological subtype of these neoplasms. Another study of stages III and IV ovarian carcinomas found a correlation between decreased survival and c-erbB-2 protein overproduction, but not between survival and histological grade.¹² One abstract stated that c-erbB-2 protein overproduction in 10 of 16 pulmonary adenocarcinomas correlated with decreased disease-free interval.⁷⁰ Another abstract described a tendency for immunohisto-

TABLE 13. c-erbB-2 ACTIVATION IN HUMAN TUMORS OF THE URINARY TRACT*

Tumor Type	c-erbB-2 DNA Amplification	c-erbB-2 mRNA Overproduction	c-erbB-2 Protein Overproduction
Kidney—renal cell carcinoma	1/5, ⁵⁷ 1/4, ¹⁰⁷ 0/5 ⁵⁴	0/16 ¹⁰⁴	—
Wilms' tumor	0/4 ⁵⁷	—	—
Prostate—adenocarcinoma	—	—	0/23 ⁵⁶
Urinary bladder—carcinoma	—	—	1/48 ⁵⁹

*Shown as number of cases with amplification (or overproduction)/total number of cases studied; reference is given as superscript. All protein studies used immunohistochemical methods.

TABLE 14. *c-erbB-2* ACTIVATION IN MISCELLANEOUS HUMAN TUMORS*

Tumor Type	<i>c-erbB-2</i> DNA Amplification	<i>c-erbB-2</i> mRNA Overproduction	<i>c-erbB-2</i> Protein Over- production
Skin—malignant melanoma	—	—	0/10 ⁸⁸
Skin, head and neck—squamous cell carcinoma	0/7 ¹⁰⁷	—	—
Site not stated—squamous cell carcinoma	0/8, ⁸⁷ 0/2 ⁷⁶	—	—
Salivary gland—adenocarcinoma	1/1 ⁷⁶	—	—
Parotid gland—adenoid cystic carcinoma	—	—	0/1 ⁶¹
Thyroid—anaplastic carcinoma	0/1 ¹	0/1 ¹	—
Thyroid—papillary carcinoma	0/5 ¹	3(low levels)/5 ¹	—
Thyroid—adenocarcinoma	0/1 ⁸⁴	—	—
Thyroid—adenoma	0/2 ¹	1(low levels)/2 ¹	—
Neuroblastoma	0/35, ⁸¹ 0/8, ⁸⁷ 0/1 ⁷⁶	—	—
Meningioma	0/2 ⁸⁷	—	—

*Shown as number of cases with amplification (or overproduction)/total number of cases studied; reference is given as superscript. All protein studies used immunohistochemical methods.

chemical reactivity for *c-erbB-2* protein to correlate with higher grades of prostatic adenocarcinoma.⁸⁷ Additional prognostic studies of ovarian carcinomas and other neoplasms are needed.

SUMMARY

Activation of the *c-erbB-2* oncogene can occur by amplification of *c-erbB-2* DNA and by overproduction of *c-erbB-2* mRNA and *c-erbB-2* protein. Approximately 20 percent of breast carcinomas show evidence of *c-erbB-2* activation, which correlates with a poor prognosis primarily in patients with metastasis to axillary lymph nodes. Studies that have attempted to correlate *c-erbB-2* activation with other prognostic factors in breast carcinoma have reported conflicting conclusions. The pathologic and clinical significance of *c-erbB-2* activation in other neoplasms is unclear and should be assessed by additional studies.

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Front cover: The photograph shows a rat nerve cell in culture. It is labeled (yellow) with a fluorescent antibody that stains its cell body and dendritic processes. Nerve terminals (green) from other neurons (not visible), which have made synapses on the cell, are labeled with a different antibody. (Courtesy of Olaf Mundigl and Pietro de Camilli.)

Dedication page: Gavin Borden, late president of Garland Publishing, weathered in during his mid-1980s climb near Mount McKinley with MBoC author Bruce Alberts and famous mountaineer guide Mugs Stump (1940–1992).

Back cover: The authors, in alphabetical order, crossing Abbey Road in London on their way to lunch. Much of this third edition was written in a house just around the corner. (Photograph by Richard Olivier.)

extracts. If these minor cell proteins differ among cells to the same extent as the more abundant proteins, as is commonly assumed, only a small number of protein differences (perhaps several hundred) suffice to create very large differences in cell morphology and behavior.

A Cell Can Change the Expression of Its Genes in Response to External Signals³

Most of the specialized cells in a multicellular organism are capable of altering their patterns of gene expression in response to extracellular cues. If a liver cell is exposed to a glucocorticoid hormone, for example, the production of several specific proteins is dramatically increased. Glucocorticoids are released during periods of starvation or intense exercise and signal the liver to increase the production of glucose from amino acids and other small molecules; the set of proteins whose production is induced includes enzymes such as tyrosine aminotransferase, which helps to convert tyrosine to glucose. When the hormone is no longer present, the production of these proteins drops to its normal level.

Other cell types respond to glucocorticoids in different ways. In fat cells, for example, the production of tyrosine aminotransferase is reduced, while some other cell types do not respond to glucocorticoids at all. These examples illustrate a general feature of cell specialization—different cell types often respond in different ways to the same extracellular signal. Underlying this specialization are features that do not change, which give each cell type its permanently distinctive character. These features reflect the persistent expression of different sets of genes.

Gene Expression Can Be Regulated at Many of the Steps in the Pathway from DNA to RNA to Protein⁴

If differences between the various cell types of an organism depend on the particular genes that the cells express, at what level is the control of gene expression exercised? There are many steps in the pathway leading from DNA to protein, and all of them can in principle be regulated. Thus a cell can control the proteins it makes by (1) controlling when and how often a given gene is transcribed (**transcriptional control**), (2) controlling how the primary RNA transcript is spliced or otherwise processed (**RNA processing control**), (3) selecting which completed mRNAs in the cell nucleus are exported to the cytoplasm (**RNA transport control**), (4) selecting which mRNAs in the cytoplasm are translated by ribosomes (**translational control**), (5) selectively destabilizing certain mRNA molecules in the cytoplasm (**mRNA degradation control**), or (6) selectively activating, inactivating, or compartmentalizing specific protein molecules after they have been made (**protein activity control**) (Figure 9-2).

For most genes transcriptional controls are paramount. This makes sense because, of all the possible control points illustrated in Figure 9-2, only transcriptional control ensures that no superfluous intermediates are synthesized. In the

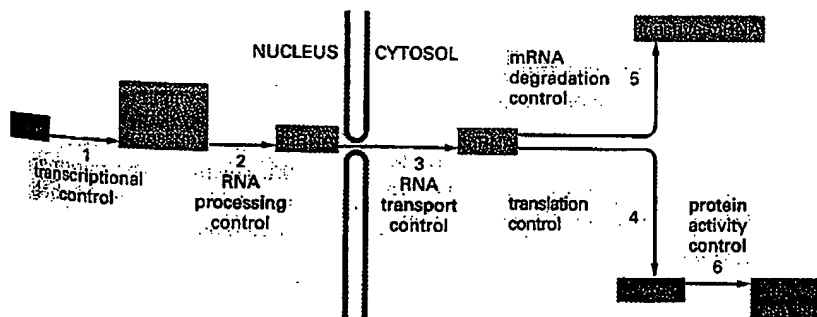


Figure 9-2 Six steps at which eucaryote gene expression can be controlled. Only controls that operate at steps 1 through 5 are discussed in this chapter. The regulation of protein activity (step 6) is discussed in Chapter 5; this includes reversible activation or inactivation by protein phosphorylation as well as irreversible inactivation by proteolytic degradation.

following sections we discuss the DNA and protein components that regulate the initiation of gene transcription. We return at the end of the chapter to the other ways of regulating gene expression.

Summary

The genome of a cell contains in its DNA sequence the information to make many thousands of different protein and RNA molecules. A cell typically expresses only a fraction of its genes, and the different types of cells in multicellular organisms arise because different sets of genes are expressed. Moreover, cells can change the pattern of genes they express in response to changes in their environment, such as signals from other cells. Although all of the steps involved in expressing a gene can in principle be regulated, for most genes the initiation of RNA transcription is the most important point of control.

DNA-binding Motifs in Gene Regulatory Proteins⁵

How does a cell determine which of its thousands of genes to transcribe? As discussed in Chapter 8, the transcription of each gene is controlled by a regulatory region of DNA near the site where transcription begins. Some regulatory regions are simple and act as switches that are thrown by a single signal. Other regulatory regions are complex and act as tiny microprocessors, responding to a variety of signals that they interpret and integrate to switch the neighboring gene on or off. Whether complex or simple, these switching devices consist of two fundamental types of components: (1) short stretches of DNA of defined sequence and (2) *gene regulatory proteins* that recognize and bind to them.

We begin our discussion of gene regulatory proteins by describing how these proteins were discovered.

Gene Regulatory Proteins Were Discovered Using Bacterial Genetics⁶

Genetic analyses in bacteria carried out in the 1950s provided the first evidence of the existence of **gene regulatory proteins** that turn specific sets of genes on or off. One of these regulators, the *lambda repressor*, is encoded by a bacterial virus, *bacteriophage lambda*. The repressor shuts off the viral genes that code for the protein components of new virus particles and thereby enables the viral genome to remain a silent passenger in the bacterial chromosome, multiplying with the bacterium when conditions are favorable for bacterial growth (see Figure 6-80). The lambda repressor was among the first gene regulatory proteins to be characterized, and it remains one of the best understood, as we discuss later. Other bacterial regulators respond to nutritional conditions by shutting off genes encoding specific sets of metabolic enzymes when they are not needed. The *lac repressor*, for example, the first of these bacterial proteins to be recognized, turns off the production of the proteins responsible for lactose metabolism when this sugar is absent from the medium.

The first step toward understanding gene regulation was the isolation of mutant strains of bacteria and bacteriophage lambda that were unable to shut off specific sets of genes. It was proposed at the time, and later proved, that most of these mutants were deficient in proteins acting as specific repressors for these sets of genes. Because these proteins, like most gene regulatory proteins, are present in small quantities, it was difficult and time-consuming to isolate them. They were eventually purified by fractionating cell extracts on a series of standard chromatography columns (see pp. 166-169). Once isolated, the proteins were shown to bind to specific DNA sequences close to the genes that they

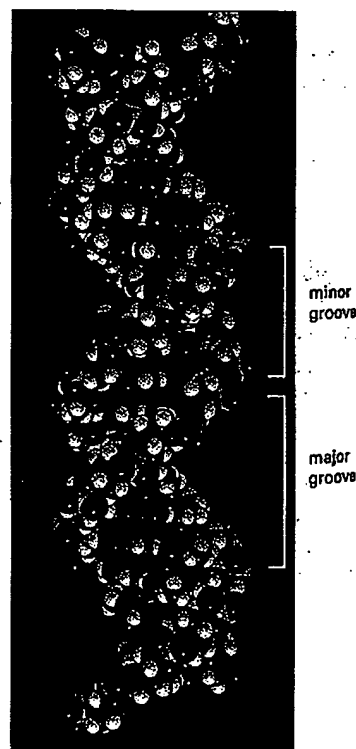
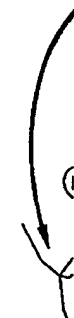
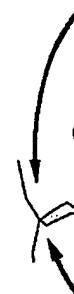


Figure 9-3 Double-helical structure of DNA. The major and minor grooves on the outside of the double helix are indicated. The atoms are colored as follows: carbon, dark blue; nitrogen, light blue; hydrogen, white; oxygen, red; phosphorus, yellow.

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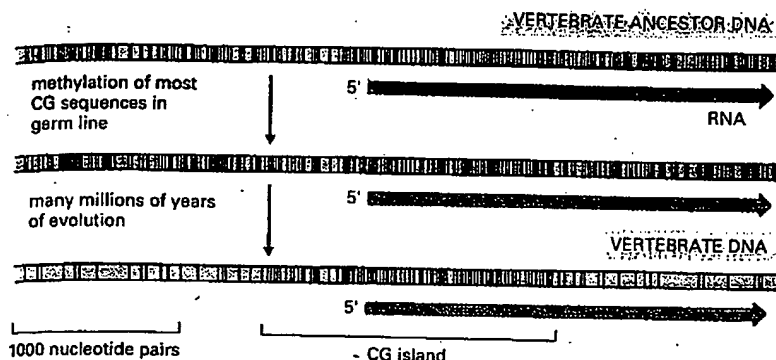


Figure 9-71 A mechanism to explain both the marked deficiency of CG sequences and the presence of CG islands in vertebrate genomes. A black line marks the location of an unmethylated CG dinucleotide in the DNA sequence, while a red line marks the location of a methylated CG dinucleotide.

Summary

The many types of cells in animals and plants are created largely through mechanisms that cause different genes to be transcribed in different cells. Since many specialized animal cells can maintain their unique character when grown in culture, the gene regulatory mechanisms involved in creating them must be stable once established and heritable when the cell divides, endowing the cell with a memory of its developmental history. Prokaryotes and yeasts provide unusually accessible model systems in which to study gene regulatory mechanisms, some of which may be relevant to the creation of specialized cell types in higher eucaryotes. One such mechanism involves a competitive interaction between two (or more) gene regulatory proteins, each of which inhibits the synthesis of the other; this can create a flip-flop switch that switches a cell between two alternative patterns of gene expression. Direct or indirect positive feedback loops, which enable gene regulatory proteins to perpetuate their own synthesis, provide a general mechanism for cell memory.

In eucaryotes gene transcription is generally controlled by combinations of gene regulatory proteins. It is thought that each type of cell in a higher eucaryotic organism contains a specific combination of gene regulatory proteins that ensures the expression of only those genes appropriate to that type of cell. A given gene regulatory protein may be expressed in a variety of circumstances and typically is involved in the regulation of many genes.

In addition to diffusible gene regulatory proteins, inherited states of chromatin condensation are also utilized by eucaryotic cells to regulate gene expression. In vertebrates DNA methylation also plays a part, mainly as a device to reinforce decisions about gene expression that are made initially by other mechanisms.

Posttranscriptional Controls

Although controls on the initiation of gene transcription are the predominant form of regulation for most genes, other controls can act later in the pathway from RNA to protein to modulate the amount of gene product that is made. Although these posttranscriptional controls, which operate after RNA polymerase has bound to the gene's promoter and begun RNA synthesis, are less common than transcriptional control, for many genes they are crucial. It seems that every step in gene expression that could be controlled in principle is likely to be regulated under some circumstances for some genes.

We consider the varieties of posttranscriptional regulation in temporal order, according to the sequence of events that might be experienced by an RNA molecule after its transcription has begun (Figure 9-72).

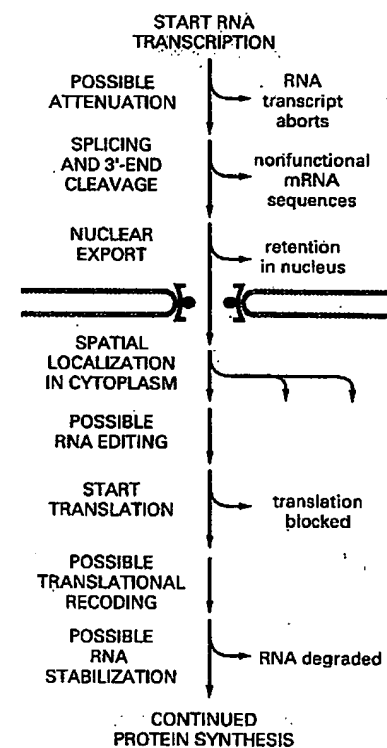


Figure 9-72 Possible posttranscriptional controls on gene expression. Only a few of these controls are likely to be used for any one gene.

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Back cover In 1967, the British artist Peter Blake created a design classic. Nearly 35 years later Nigel Orme (illustrator), Richard Denyer (photographer), and the authors have together produced an affectionate tribute to Mr Blake's image. With its gallery of icons and influences, its assembly created almost as much complexity, intrigue and mystery as the original. *Drosophila*, *Arabidopsis*, Dolly and the assembled company tempt you to dip inside where, as in the original, "a splendid time is guaranteed for all." (Gunter Blobel, courtesy of The Rockefeller University; Marie Curie, Keystone Press Agency Inc; Darwin bust, by permission of the President and Council of the Royal Society; Rosalind Franklin, courtesy of Cold Spring Harbor Laboratory Archives; Dorothy Hodgkin, © The Nobel Foundation, 1984; James Joyce, etching by Peter Blake; Robert Johnson, photo booth self-portrait early 1930s, © 1986 Delta Haze Corporation all rights reserved, used by permission; Albert L. Lehninger, (unidentified photographer) courtesy of The Alan Mason Chesney Medical Archives of The Johns Hopkins Medical Institutions; Linus Pauling, from Ava Helen and Linus Pauling Papers, Special Collections, Oregon State University; Nicholas Poussin, courtesy of ArtToday.com; Barbara McClintock, © David Micklos, 1983; Andrei Sakharov, courtesy of Elena Bonner; Frederick Sanger, © The Nobel Foundation, 1958.)

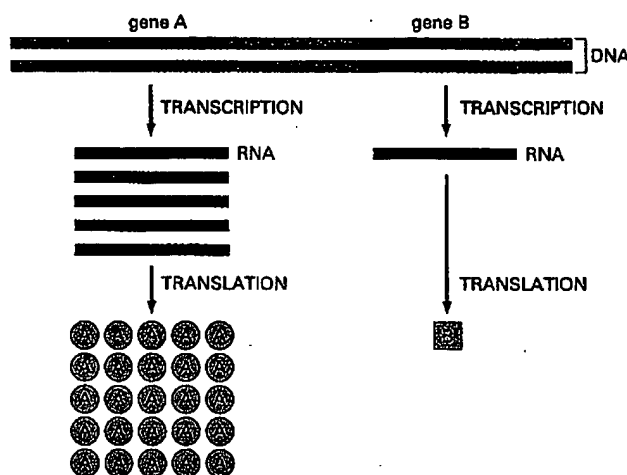


Figure 6-3 Genes can be expressed with different efficiencies. Gene A is transcribed and translated much more efficiently than gene B. This allows the amount of protein A in the cell to be much greater than that of protein B.

FROM DNA TO RNA

Transcription and translation are the means by which cells read out, or express, the genetic instructions in their genes. Because many identical RNA copies can be made from the same gene, and each RNA molecule can direct the synthesis of many identical protein molecules, cells can synthesize a large amount of protein rapidly when necessary. But each gene can also be transcribed and translated with a different efficiency, allowing the cell to make vast quantities of some proteins and tiny quantities of others (Figure 6-3). Moreover, as we see in the next chapter, a cell can change (or regulate) the expression of each of its genes according to the needs of the moment—most obviously by controlling the production of its RNA.

Portions of DNA Sequence Are Transcribed into RNA

The first step a cell takes in reading out a needed part of its genetic instructions is to copy a particular portion of its DNA nucleotide sequence—a gene—into an RNA nucleotide sequence. The information in RNA, although copied into another chemical form, is still written in essentially the same language as it is in DNA—the language of a nucleotide sequence. Hence the name **transcription**.

Like DNA, RNA is a linear polymer made of four different types of nucleotide subunits linked together by phosphodiester bonds (Figure 6-4). It differs from DNA chemically in two respects: (1) the nucleotides in RNA are *ribonucleotides*—that is, they contain the sugar ribose (hence the name *ribonucleic acid*) rather than deoxyribose; (2) although, like DNA, RNA contains the bases adenine (A), guanine (G), and cytosine (C), it contains the base uracil (U) instead of the thymine (T) in DNA. Since U, like T, can base-pair by hydrogen-bonding with A (Figure 6-5), the complementary base-pairing properties described for DNA in Chapters 4 and 5 apply also to RNA (in RNA, G pairs with C, and A pairs with U). It is not uncommon, however, to find other types of base pairs in RNA: for example, G pairing with U occasionally.

Despite these small chemical differences, DNA and RNA differ quite dramatically in overall structure. Whereas DNA always occurs in cells as a double-stranded helix, RNA is single-stranded. RNA chains therefore fold up into a variety of shapes, just as a polypeptide chain folds up to form the final shape of a protein (Figure 6-6). As we see later in this chapter, the ability to fold into complex three-dimensional shapes allows some RNA molecules to have structural and catalytic functions.

Transcription Produces RNA Complementary to One Strand of DNA

All of the RNA in a cell is made by DNA transcription, a process that has certain similarities to the process of DNA replication discussed in Chapter 5.

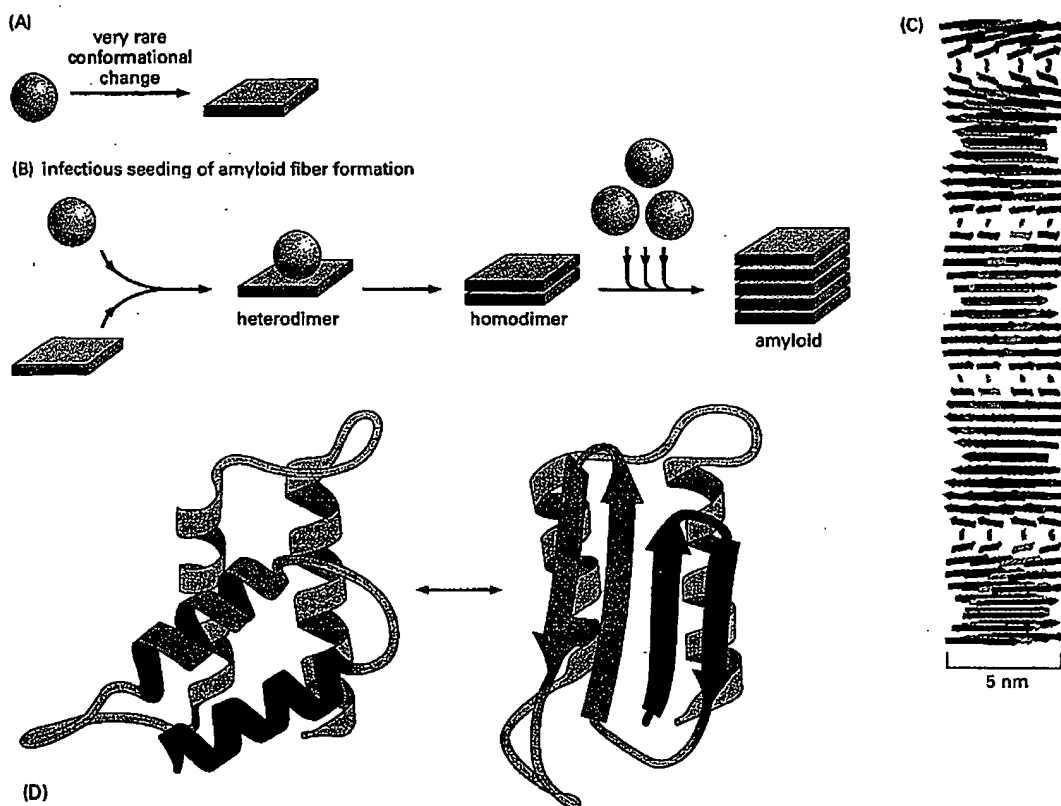


Figure 6-89 Protein aggregates that cause human disease. (A) Schematic illustration of the type of conformational change in a protein that produces material for a cross-beta filament. (B) Diagram illustrating the self-infectious nature of the protein aggregation that is central to prion diseases. PrP is highly unusual because the misfolded version of the protein, called PrP^{*}, induces the normal PrP protein it contacts to change its conformation, as shown. Most of the human diseases caused by protein aggregation are caused by the overproduction of a variant protein that is especially prone to aggregation, but because this structure is not infectious in this way, it cannot spread from one animal to another. (C) Drawing of a cross-beta filament, a common type of protease-resistant protein aggregate found in a variety of human neurological diseases. Because the hydrogen-bond interactions in a β sheet form between polypeptide backbone atoms (see Figure 3-9), a number of different abnormally folded proteins can produce this structure. (D) One of several possible models for the conversion of PrP to PrP^{*}, showing the likely change of two α -helices into four β -strands. Although the structure of the normal protein has been determined accurately, the structure of the infectious form is not yet known with certainty because the aggregation has prevented the use of standard structural techniques. (C, courtesy of Louise Serpell, adapted from M. Sunde et al., *J. Mol. Biol.* 273:729-739, 1997; D, adapted from S.B. Prusiner, *Trends Biochem. Sci.* 21:482-487, 1996.)

animals and humans. It can be dangerous to eat the tissues of animals that contain PrP^{*}, as witnessed most recently by the spread of BSE (commonly referred to as the "mad cow disease") from cattle to humans in Great Britain.

Fortunately, in the absence of PrP^{*}, PrP is extraordinarily difficult to convert to its abnormal form. Although very few proteins have the potential to misfold into an infectious conformation, a similar transformation has been discovered to be the cause of an otherwise mysterious "protein-only inheritance" observed in yeast cells.

There Are Many Steps From DNA to Protein

We have seen so far in this chapter that many different types of chemical reactions are required to produce a properly folded protein from the information contained in a gene (Figure 6-90). The final level of a properly folded protein in a cell therefore depends upon the efficiency with which each of the many steps is performed.

We discuss in Chapter 7 that cells have the ability to change the levels of their proteins according to their needs. In principle, any or all of the steps in Fig-

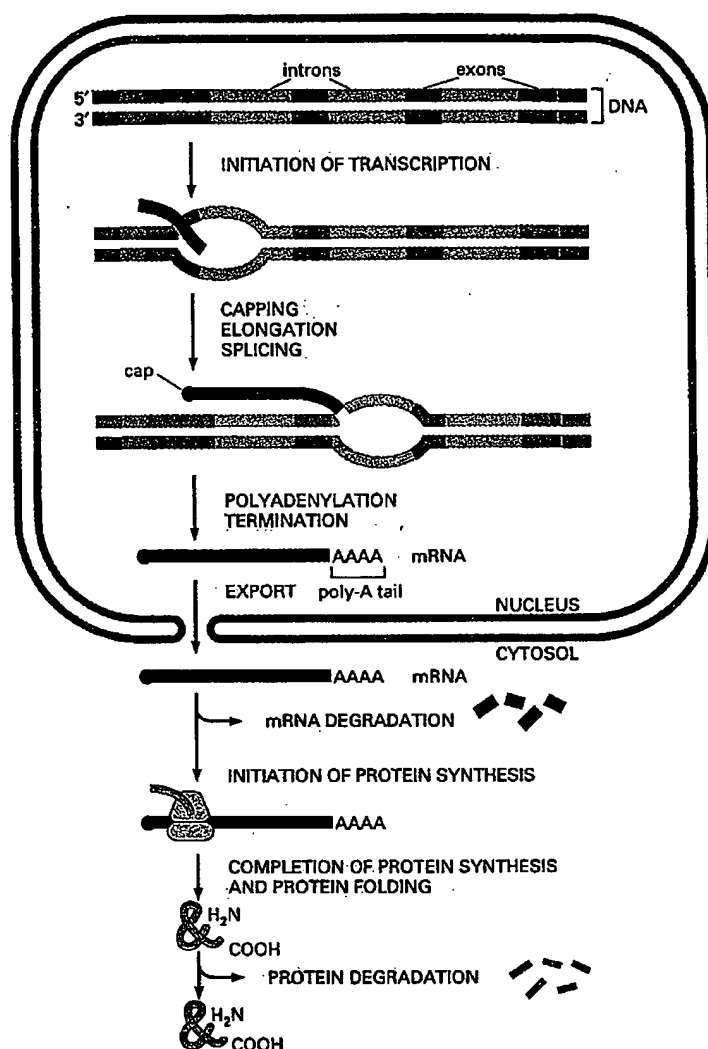


Figure 6-90 The production of a protein by a eucaryotic cell. The final level of each protein in a eucaryotic cell depends upon the efficiency of each step depicted.

ure 6-90) could be regulated by the cell for each individual protein. However, as we shall see in Chapter 7, the initiation of transcription is the most common point for a cell to regulate the expression of each of its genes. This makes sense, inasmuch as the most efficient way to keep a gene from being expressed is to block the very first step—the transcription of its DNA sequence into an RNA molecule.

Summary

The translation of the nucleotide sequence of an mRNA molecule into protein takes place in the cytoplasm on a large ribonucleoprotein assembly called a ribosome. The amino acids used for protein synthesis are first attached to a family of tRNA molecules, each of which recognizes, by complementary base-pair interactions, particular sets of three nucleotides in the mRNA (codons). The sequence of nucleotides in the mRNA is then read from one end to the other in sets of three according to the genetic code.

To initiate translation, a small ribosomal subunit binds to the mRNA molecule at a start codon (AUG) that is recognized by a unique initiator tRNA molecule. A large ribosomal subunit binds to complete the ribosome and begin the elongation phase of protein synthesis. During this phase, aminoacyl tRNAs—each bearing a specific amino acid bind sequentially to the appropriate codon in mRNA by forming complementary base pairs with the tRNA anticodon. Each amino acid is added to the C-terminal end of the growing polypeptide by means of a cycle of three sequential

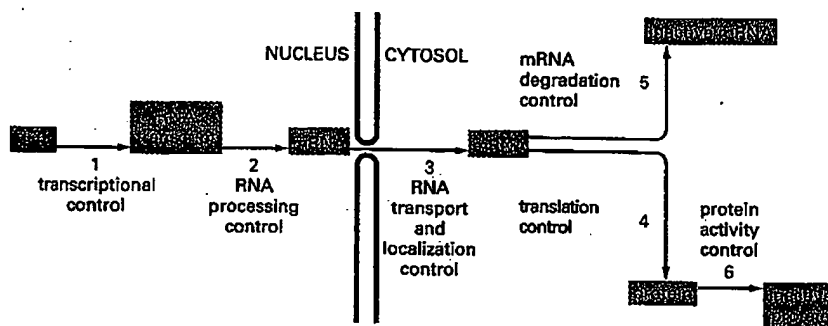


Figure 7-5 Six steps at which eucaryotic gene expression can be controlled. Controls that operate at steps 1 through 5 are discussed in this chapter. Step 6, the regulation of protein activity, includes reversible activation or inactivation by protein phosphorylation (discussed in Chapter 3) as well as irreversible inactivation by proteolytic degradation (discussed in Chapter 6).

Gene Expression Can Be Regulated at Many of the Steps in the Pathway from DNA to RNA to Protein

If differences among the various cell types of an organism depend on the particular genes that the cells express, at what level is the control of gene expression exercised? As we saw in the last chapter, there are many steps in the pathway leading from DNA to protein, and all of them can in principle be regulated. Thus a cell can control the proteins it makes by (1) controlling when and how often a given gene is transcribed (**transcriptional control**), (2) controlling how the RNA transcript is spliced or otherwise processed (**RNA processing control**), (3) selecting which completed mRNAs in the cell nucleus are exported to the cytosol and determining where in the cytosol they are localized (**RNA transport and localization control**), (4) selecting which mRNAs in the cytoplasm are translated by ribosomes (**translational control**), (5) selectively destabilizing certain mRNA molecules in the cytoplasm (**mRNA degradation control**), or (6) selectively activating, inactivating, degrading, or compartmentalizing specific protein molecules after they have been made (**protein activity control**) (Figure 7-5).

For most genes transcriptional controls are paramount. This makes sense because, of all the possible control points illustrated in Figure 7-5, only transcriptional control ensures that the cell will not synthesize superfluous intermediates. In the following sections we discuss the DNA and protein components that perform this function by regulating the initiation of gene transcription. We shall return at the end of the chapter to the additional ways of regulating gene expression.

Summary

The genome of a cell contains in its DNA sequence the information to make many thousands of different protein and RNA molecules. A cell typically expresses only a fraction of its genes, and the different types of cells in multicellular organisms arise because different sets of genes are expressed. Moreover, cells can change the pattern of genes they express in response to changes in their environment, such as signals from other cells. Although all of the steps involved in expressing a gene can in principle be regulated, for most genes the initiation of RNA transcription is the most important point of control.

DNA-BINDING MOTIFS IN GENE REGULATORY PROTEINS

How does a cell determine which of its thousands of genes to transcribe? As mentioned briefly in Chapters 4 and 6, the transcription of each gene is controlled by a regulatory region of DNA relatively near the site where transcription begins. Some regulatory regions are simple and act as switches that are thrown by a single signal. Many others are complex and act as tiny microprocessors, responding to a variety of signals that they interpret and integrate to switch the neighboring gene on or off. Whether complex or simple, these switching devices

occur in the germ line, the cell lineage that gives rise to sperm or eggs. Most of the DNA in vertebrate germ cells is inactive and highly methylated. Over long periods of evolutionary time, the methylated CG sequences in these inactive regions have presumably been lost through spontaneous deamination events that were not properly repaired. However promoters of genes that remain active in the germ cell lineages (including most housekeeping genes) are kept unmethylated, and therefore spontaneous deaminations of Cs that occur within them can be accurately repaired. Such regions are preserved in modern day vertebrate cells as CG islands. In addition, any mutation of a CG sequence in the genome that destroyed the function or regulation of a gene in the adult would be selected against, and some CG islands are simply the result of a higher than normal density of critical CG sequences.

The mammalian genome contains an estimated 20,000 CG islands. Most of the islands mark the 5' ends of transcription units and thus, presumably, of genes. The presence of CG islands often provides a convenient way of identifying genes in the DNA sequences of vertebrate genomes.

Summary

The many types of cells in animals and plants are created largely through mechanisms that cause different genes to be transcribed in different cells. Since many specialized animal cells can maintain their unique character through many cell division cycles and even when grown in culture, the gene regulatory mechanisms involved in creating them must be stable once established and heritable when the cell divides. These features endow the cell with a memory of its developmental history. Bacteria and yeasts provide unusually accessible model systems in which to study gene regulatory mechanisms. One such mechanism involves a competitive interaction between two gene regulatory proteins, each of which inhibits the synthesis of the other; this can create a flip-flop switch that switches a cell between two alternative patterns of gene expression. Direct or indirect positive feedback loops, which enable gene regulatory proteins to perpetuate their own synthesis, provide a general mechanism for cell memory. Negative feedback loops with programmed delays form the basis for cellular clocks.

In eucaryotes the transcription of a gene is generally controlled by combinations of gene regulatory proteins. It is thought that each type of cell in a higher eucaryotic organism contains a specific combination of gene regulatory proteins that ensures the expression of only those genes appropriate to that type of cell. A given gene regulatory protein may be active in a variety of circumstances and typically is involved in the regulation of many genes.

In addition to diffusible gene regulatory proteins, inherited states of chromatin condensation are also used by eucaryotic cells to regulate gene expression. An especially dramatic case is the inactivation of an entire X chromosome in female mammals. In vertebrates DNA methylation also functions in gene regulation, being used mainly as a device to reinforce decisions about gene expression that are made initially by other mechanisms. DNA methylation also underlies the phenomenon of genomic imprinting in mammals, in which the expression of a gene depends on whether it was inherited from the mother or the father.

POSTTRANSCRIPTIONAL CONTROLS

In principle, every step required for the process of gene expression could be controlled. Indeed, one can find examples of each type of regulation, although any one gene is likely to use only a few of them. Controls on the initiation of gene transcription are the predominant form of regulation for most genes. But other controls can act later in the pathway from DNA to protein to modulate the amount of gene product that is made. Although these posttranscriptional controls, which operate after RNA polymerase has bound to the gene's promoter and begun RNA synthesis, are less common than transcriptional control, for many genes they are crucial.

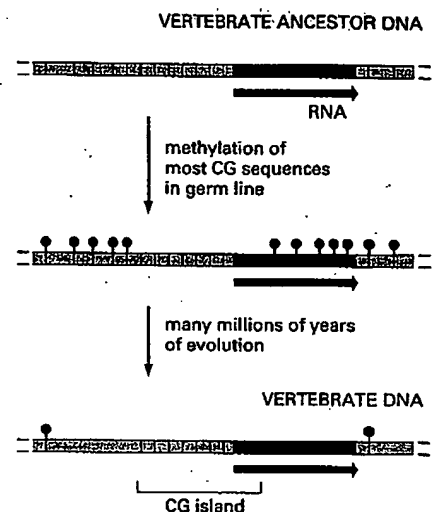


Figure 7-86 A mechanism to explain both the marked overall deficiency of CG sequences and their clustering into CG islands in vertebrate genomes. A black line marks the location of a CG dinucleotide in the DNA sequence, while a red "lollipop" indicates the presence of a methyl group on the CG dinucleotide. CG sequences that lie in regulatory sequences of genes that are transcribed in germ cells are unmethylated and therefore tend to be retained in evolution. Methylated CG sequences, on the other hand, tend to be lost through deamination of 5-methyl C to T, unless the CG sequence is critical for survival.

CHAPTER 29

Regulation of transcription

Genes VI (1997) CH 29, pp. 847-848.
Benjamin Lewin

The phenotypic differences that distinguish the various kinds of cells in a higher eukaryote are largely due to differences in the expression of genes that code for proteins, that is, those transcribed by RNA polymerase II. In principle, the expression of these genes might be regulated at any one of several stages. The concept of the "level of control" implies that gene expression is not necessarily an automatic process once it has begun. It could be regulated in a gene-specific way at any one of several sequential steps. We can distinguish (at least) five potential control points, forming the series:

Activation of gene structure
↓
Initiation of transcription
↓
Processing the transcript
↓
Transport to cytoplasm
↓
Translation of mRNA

The existence of the first step is implied by the discovery that genes may exist in either of two structural conditions. Relative to the state of most of the genome, genes are found in an "active" state in the cells in which they are expressed (see Chapter 27). The change of structure is distinct from the act of transcription, and indicates that the gene is "transcribable." This suggests that acquisition of the "active" structure must be the first step in gene expression.

Transcription of a gene in the active state is

controlled at the stage of initiation, that is, by the interaction of RNA polymerase with its promoter. This is now becoming susceptible to analysis in the *in vitro* systems (see Chapter 28). For most genes, this is a major control point; probably it is the most common level of regulation.

There is at present no evidence for control at subsequent stages of transcription in eukaryotic cells, for example, via antitermination mechanisms.

The primary transcript is modified by capping at the 5' end, and usually also by polyadenylation at the 3' end. Introns must be spliced out from the transcripts of interrupted genes. The mature RNA must be exported from the nucleus to the cytoplasm. Regulation of gene expression by selection of sequences at the level of nuclear RNA might involve any or all of these stages, but the one for which we have most evidence concerns changes in splicing: some genes are expressed by means of alternative splicing patterns whose regulation controls the type of protein product (see Chapter 30).

Finally, the translation of an mRNA in the cytoplasm can be specifically controlled. There is little evidence for the employment of this mechanism in adult somatic cells, but it does occur in some embryonic situations, as described in Chapter 7. The mechanism is presumed to involve the blocking of initiation of translation of some mRNAs by specific protein factors.

But having acknowledged that control of gene expression can occur at multiple stages, and that production of RNA cannot inevitably be equated with production of protein; it is clear

that the overwhelming majority of regulatory events occur at the initiation of transcription. Regulation of tissue-specific gene transcription lies at the heart of eukaryotic differentiation; indeed, we see examples in Chapter 38 in which proteins that regulate embryonic development prove to be transcription factors. A regulatory transcription factor serves to provide

common control of a large number of target genes, and we seek to answer two questions about this mode of regulation: what identifies the common target genes to the transcription factor; and how is the activity of the transcription factor itself regulated in response to intrinsic or extrinsic signals?

Response elements identify genes under common regulation

The principle that emerges from characterizing groups of genes under common control is that *they share a promoter element that is recognized by a regulatory transcription factor*. An element that causes a gene to respond to such a factor is called a response element; examples are the HSE (heat shock response element), GRE (glucocorticoid response element), SRE (serum response element).

The properties of some inducible transcription factors and the elements that they recognize are summarized in Table 29.1. Response elements have the same general characteristics as upstream elements of promoters or enhancers. They contain short consensus sequences, and copies of the response elements found in different genes are closely related, but not necessarily identical. The region bound by the factor extends for a short distance on either side of

the consensus sequence. In promoters, the elements are not present at fixed distances from the startpoint, but are usually <200 bp upstream of it. The presence of a single element usually is sufficient to confer the regulatory response, but sometimes there are multiple copies.

Response elements may be located in promoters or in enhancers. Some types of elements are typically found in one rather than the other: usually an HSE is found in a promoter, while a GRE is found in an enhancer. We assume that all response elements function by the same general principle. *A gene is regulated by a sequence at the promoter or enhancer that is recognized by a specific protein. The protein functions as a transcription factor needed for RNA polymerase to initiate. Active protein is available only under conditions when the gene is to be expressed; its absence means that the promoter is not activated by this particular circuit.*

An example of a situation in which many genes are controlled by a single factor is provided by the heat shock response. This is common to a wide range of prokaryotes and eukaryotes and involves multiple controls of gene expression: an increase in temperature turns off transcription of some genes, turns on transcription of the heat shock genes, and causes changes in the translation of mRNAs. The control of the heat shock genes illustrates the differences between prokaryotic and eukaryotic modes of control. In bacteria, a new sigma factor is synthesized that directs RNA polymerase holoenzyme to recognize an alter-

Table 29.1 Inducible transcription factors bind to response elements that identify groups of promoters or enhancers subject to coordinate control.

Regulatory Agent	Module	Consensus	Factor
Heat shock	HSE	CNNGAANNTCCNNG	HSTF
Glucocorticoid	GRE	TGGTACAAATGTTCT	Receptor
Phorbol ester	TRE	TGACTCA	AP1
Serum	SRE	CCATATTAGG	SRF

Research

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Prostate stem cell antigen (PSCA) expression in human prostate cancer tissues and its potential role in prostate carcinogenesis and progression of prostate cancer

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Abstract

Background: Prostate stem cell antigen (PSCA) is a recently defined homologue of the Thy-1/Ly-6 family of glycosylphosphatidylinositol (GPI)-anchored cell surface antigens. The purpose of the present study was to examine the expression status of PSCA protein and mRNA in clinical specimens of human prostate cancer (Pca) and to validate it as a potential molecular target for diagnosis and treatment of Pca.

Materials and Methods: Immunohistochemical (IHC) and *in situ* hybridization (ISH) analyses of PSCA expression were simultaneously performed on paraffin-embedded sections from 20 benign prostatic hyperplasia (BPH), 20 prostatic intraepithelial neoplasia (PIN) and 48 prostate cancer (Pca) tissues, including 9 androgen-independent prostate cancers. The level of PSCA expression was semiquantitatively scored by assessing both the percentage and intensity of PSCA-positive staining cells in the specimens. Then compared PSCA expression between BPH, PIN and Pca tissues and analysed the correlations of PSCA expression level with pathological grade, clinical stage and progression to androgen-independence in Pca.

Results: In BPH and low grade PIN, PSCA protein and mRNA staining were weak or negative and less intense and uniform than that seen in HGPIN and Pca. There were moderate to strong PSCA protein and mRNA expression in 8 of 11 (72.7%) HGPIN and in 40 of 48 (83.4%) Pca specimens examined by IHC and ISH analyses, with statistical significance compared with BPH (20%) and low grade PIN (22.2%) samples ($p < 0.05$, respectively). The expression level of PSCA increased with high Gleason grade, advanced stage and progression to androgen-independence ($p < 0.05$, respectively). In addition, IHC and ISH staining showed a high degree of correlation between PSCA protein and mRNA overexpression.

Conclusions: Our data demonstrate that PSCA as a new cell surface marker is overexpressed by a majority of human Pca. PSCA expression correlates positively with adverse tumor characteristics, such as increasing pathological grade (poor cell differentiation), worsening clinical stage and androgen-independence, and speculatively with prostate carcinogenesis. PSCA protein overexpression results from upregulated transcription of PSCA mRNA. PSCA may have prognostic utility and may be a promising molecular target for diagnosis and treatment of Pca.

Introduction

Prostate cancer (Pca) is the second leading cause of cancer-related death in American men and is becoming a common cancer increasing in China. Despite recently great progress in the diagnosis and management of localized disease, there continues to be a need for new diagnostic markers that can accurately discriminate between indolent and aggressive variants of Pca. There also continues to be a need for the identification and characterization of potential new therapeutic targets on Pca cells. Current diagnostic and therapeutic modalities for recurrent and metastatic Pca have been limited by a lack of specific target antigens of Pca.

Although a number of prostate-specific genes have been identified (i.e. prostate specific antigen, prostatic acid phosphatase, glandular kallikrein 2), the majority of these are secreted proteins not ideally suited for many immunological strategies. So, the identification of new cell surface antigens is critical to the development of new diagnostic and therapeutic approaches to the management of Pca.

Reiter RE et al [1] reported the identification of prostate stem cell antigen (PSCA), a cell surface antigen that is predominantly prostate specific. The PSCA gene encodes a 123 amino acid glycoprotein, with 30% homology to stem cell antigen 2 (Sca 2). Like Sca-2, PSCA also belongs to a member of the Thy-1/Ly-6 family and is anchored by a glycosylphosphatidylinositol (GPI) linkage. mRNA *in situ* hybridization (ISH) localized PSCA expression in normal prostate to the basal cell epithelium, the putative stem cell compartment of prostatic epithelium, suggesting that PSCA may be a marker of prostate stem/progenitor cells.

In order to examine the status of PSCA protein and mRNA expression in human Pca and validate it as a potential diagnostic and therapeutic target for Pca, we used immunohistochemistry (IHC) and *in situ* hybridization (ISH) simultaneously, and conducted PSCA protein and mRNA expression analyses in paraffin-embedded tissue specimens of benign prostatic hyperplasia (BPH, n = 20), prostate intraepithelial neoplasm (PIN, n = 20) and prostate cancer (Pca, n = 48). Furthermore, we evaluated the possible correlation of PSCA expression level with Pca tumorigenesis, grade, stage and progression to androgen-independence.

Materials and methods

Tissue samples

All of the clinical tissue specimens studied herein were obtained from 80 patients of 57–84 years old by prostatectomy, transurethral resection of prostate (TURP) or biopsies. The patients were classified as 20 cases of BPH, 20 cases of PIN, 40 cases of primary Pca, including 9 patients

with recurrent Pca and a history of androgen ablation therapy (orchiectomy and/or hormonal therapy), who were referred to as androgen-independent prostate cancers. Eight specimens were harvested from these androgen-independent Pca patients prior to androgen ablation treatment. Each tissue sample was cut into two parts, one was fixed in 10% formalin for IHC and the other treated with 4% paraformaldehyde/0.1 M PBS PH 7.4 in 0.1% DEPC for 1 h for ISH analysis, and then embedded in paraffin. All paraffin blocks examined were then cut into 5 μ m sections and mounted on the glass slides specific for IHC and ISH respectively in the usual fashion. H&E-stained section of each Pca was evaluated and assigned a Gleason score by the experienced urological pathologist at our institution based on the criteria of Gleason score [2]. The Gleason sums are summarized in Table 1. Clinical staging was performed according to Jewett-whitmore-prout staging system, as shown in Table 2. In the category of PIN, we graded the specimens into two groups, i.e. low grade PIN (grade I – II) and high grade PIN (HGPN, grade III) on the basis of literatures [3,4].

Immunohistochemical (IHC) analysis

Briefly, tissue sections were deparaffinized, dehydrated, and subjected to microwaving in 10 mmol/L citrate buffer, PH 6.0 (Boshide, Wuhan, China) in a 900 W oven for 5 min to induce epitope retrieval. Slides were allowed to cool at room temperature for 30 min. A primary mouse antibody specific to human PSCA (Boshide, Wuhan, China) with a 1:100 dilution was applied to incubate with the slides at room temperature for 2 h. Labeling was detected by sequentially adding biotinylated secondary antibodies and streptavidin-peroxidase, and localized using 3,3'-diaminobenzidine reaction. Sections were then counterstained with hematoxylin. Substitution of the primary antibody with phosphate-buffered-saline (PBS) served as a negative-staining control.

mRNA *in situ* hybridization (ISH)

Five- μ m-thick tissue sections were deparaffinized and dehydrated, then digested in pepsin solution (4 mg/ml in 3% citric acid) for 20 min at 37.5°C, and further processed for ISH. Digoxigenin-labeled sense and antisense human PSCA RNA probes (obtained from Boshide, Wuhan, China) were hybridized to the sections at 48°C overnight. The posthybridization wash with a high stringency was performed sequentially at 37°C in 2 \times standard saline citrate (SSC) for 10 min, in 0.5 \times SSC for 15 min and in 0.2 \times SSC for 30 min. The slides were then incubated to biotinylated mouse anti-digoxigenin antibody at 37.5°C for 1 h followed by washing in 1 \times PBS for 20 min at room temperature, and then to streptavidin-peroxidase at 37.5°C for 20 min followed by washing in 1 \times PBS for 15 min at room temperature. Subsequently, the slides were developed with diaminobenzidine and then coun-

Table 1: Correlation of PSCA expression with Gleason score

Gleason score	Intensity × frequency	
	0-6 (%)	9 (%)
2-4	5 (83)	1 (17)
5-7	19 (79)	5 (21)
8-10	5 (28)	13 (72)

Table 2: Correlation of PSCA expression with clinical stage

Tumor stage	Intensity × frequency	
	0-6 (%)	9 (%)
≤B	27 (67.5)	13 (32.5)
≥C	2 (25)	6 (75)

terstained with hematoxylin to localize the hybridization signals. Sections hybridized with the sense control probes routinely did not show any specific hybridization signal above background. All slides were hybridized with PBS to substitute for the probes as a negative control.

Scoring methods

To determine the correlation between the results of PSCA immunostaining and mRNA *in situ* hybridization, the same scoring manners are taken in the present study for PSCA protein staining by IHC and PSCA mRNA staining by ISH. Each slide was read and scored by two independently experienced urological pathologists using Olympus BX-41 light microscopes. The evaluation was done in a blinded fashion. For each section, five areas of similar grade were analyzed semiquantitatively for the fraction of cells staining. Fifty percent of specimens were randomly chosen and rescored to determine the degree of interobserver and intraobserver concordance. There was greater than 95% intra- and interobserver agreement.

The intensity of PSCA expression evaluated microscopically was graded on a scale of 0 to 3+ with 3 being the highest expression observed (0, no staining; 1+, mildly intense; 2+, moderately intense; 3+, severely intense). The staining density was quantified as the percentage of cells staining positive for PSCA with the primary antibody or hybridization probe, as follows: 0 = no staining; 1 = positive staining in <25% of the sample; 2 = positive staining in 25%-50% of the sample; 3 = positive staining in >50%

of the sample. Intensity score (0 to 3+) was multiplied by the density score (0-3) to give an overall score of 0-9 [1,5]. In this way, we were able to differentiate specimens that may have had focal areas of increased staining from those that had diffuse areas of increased staining [6]. The overall score for each specimen was then categorically assigned to one of the following groups: 0 score, negative expression; 1-2 scores, weak expression; 3-6 scores, moderate expression; 9 score, strong expression.

Statistical analysis

Intensity and density of PSCA protein and mRNA expression in BPH, PIN and Pca tissues were compared using the Chi-square and Student's *t*-test. Univariate associations between PSCA expression and Gleason score, clinical stage and progression to androgen-independence were calculated using Fisher's Exact Test. For all analyses, *p* < 0.05 was considered statistically significant.

Results

PSCA expression in BPH

In general, PSCA protein and mRNA were expressed weakly in individual samples of BPH. Some areas of prostate expressed weak levels (composite score 1-2), whereas other areas were completely negative (composite score 0). Four cases (20%) of BPH had moderate expression of PSCA protein and mRNA (composite score 4-6) by IHC and ISH. In 2/20 (10%) BPH specimens, PSCA mRNA expression was moderate (composite score 3-6), but PSCA protein expression was weak (composite score

2) in one and negative (composite score 0) in the other. PSCA expression was localized to the basal and secretory epithelial cells, and prostatic stroma was almost negative staining for PSCA protein and mRNA in all cases examined.

PSCA expression in PIN

In this study, we detected weak or negative expression of PSCA protein and mRNA (≤ 2 scores) in 7 of 9 (77.8%) low grade PIN and in 2 of 11 (18.2%) HGPIN, and moderate expression (3–6 scores) in the rest 2 low grade PIN and 5 of 11 (45.5%) HGPIN. One HGPIN with moderate PSCA mRNA expression (6 score) was found weak staining for PSCA protein (2 score) by IHC. Strong PSCA protein and mRNA expression (9 score) were detected in the remaining 3 of 11 (27.3%) HGPIN. There was a statistically significant difference of PSCA protein and mRNA expression levels observed between HGPIN and BPH ($p < 0.05$), but no statistical difference reached between low grade PIN and BPH ($p > 0.05$).

PSCA expression in Pca

In order to determine if PSCA protein and mRNA can be detected in prostate cancers and if PSCA expression levels are increased in malignant compared with benign glands, Forty-eight paraffin-embedded Pca specimens were analysed by IHC and ISH. It was shown that 19 of 48 (39.6%) Pca samples stained very strongly for PSCA protein and mRNA with a score of 9 and another 21 (43.8%) specimens displayed moderate staining with scores of 4–6 (Figure 1). In addition, 4 specimens with moderate to strong PSCA mRNA expression (scores of 4–9) had weak protein staining (a score of 2) by IHC analyses. Overall, Pca expressed a significantly higher level of PSCA protein and mRNA than any other specimen category in this study ($p < 0.05$, compared with BPH and PIN respectively). The result demonstrates that PSCA protein and mRNA are overexpressed by a majority of human Pca.

Correlation of PSCA expression with Gleason score in Pca

Using the semi-quantitative scoring method as described in Materials and Methods, we compared the expression level of PSCA protein and mRNA with Gleason grade of Pca, as shown in Table 1. Prostate adenocarcinomas were graded by Gleason score as 2–4 scores = well-differentiation, 5–7 scores = moderate-differentiation and 8–10 scores = poor-differentiation [7]. Seventy-two percent of Gleason scores 8–10 prostate cancers had very strong staining of PSCA compared to 21% with Gleason scores 5–7 and 17% with 2–4 respectively, demonstrating that poorly differentiated Pca had significantly stronger expression of PSCA protein and mRNA than moderately and well differentiated tumors ($p < 0.05$). As depicted in Figure 1, IHC and ISH analyses showed that PSCA protein and mRNA expression in several cases of poorly differen-

tiated Pca were particularly prominent, with more intense and uniform staining. The results indicate that PSCA expression increases significantly with higher tumor grade in human Pca.

Correlation of PSCA expression with clinical stage in Pca

With regards to PSCA expression in every stage of Pca, we showed the results in Table 2. Seventy-five percent of locally advanced and node positive cancers (i.e. C-D stages) expressed statistically high levels of PSCA versus 32.5% that were organ confined (i.e. A-B stages) ($p < 0.05$). The data demonstrate that PSCA expression increases significantly with advanced tumor stage in human Pca.

Correlation of PSCA expression with androgen-independent progression of Pca

All 9 specimens of androgen-independent prostate cancers stained positive for PSCA protein and mRNA. Eight specimens were obtained from patients managed prior to androgen ablation therapy. Seven of eight (87.5%) of these androgen-independent prostate cancers were in the strongest staining category (score = 9), compared with three out of eight (37.5%) of patients with androgen-dependent cancers ($p < 0.05$). The results demonstrate that PSCA expression increases significantly with progression to androgen-independence of human Pca.

It is evident from the results above that within a majority of human prostate cancers the level of PSCA protein and mRNA expression correlates significantly with increasing grade, worsening stage and progression to androgen-independence.

Correlation of PSCA Immunostaining and mRNA in situ hybridization

In all 88 specimens surveyed herein, we compared the results of PSCA IHC staining with mRNA ISH analysis. Positive staining areas and its intensity and density scores evaluated by IHC were identical to those seen by ISH in 79 of 88 (89.8%) specimens (18/20 BPH, 19/20 PIN and 42/48 Pca respectively). Importantly, 27/27 samples with PSCA mRNA composite scores of 0–2, 32/36 samples with scores of 3–6 and 22/24 samples with a score of 9 also had PSCA protein expression scores of 0–2, 3–6 and 9 respectively. However, in 5 samples with PSCA mRNA overall scores of 3–6 and in 2 with scores of 9 there were less or negative PSCA protein expression (i.e. scores of 0–4), suggesting that this may reflect posttranscriptional modification of PSCA or that the epitopes recognized by PSCA mAb may be obscured in some cancers. The data demonstrate that the results of PSCA immunostaining were consistent with those of mRNA ISH analysis, showing a high degree of correlation between PSCA protein and mRNA expression.

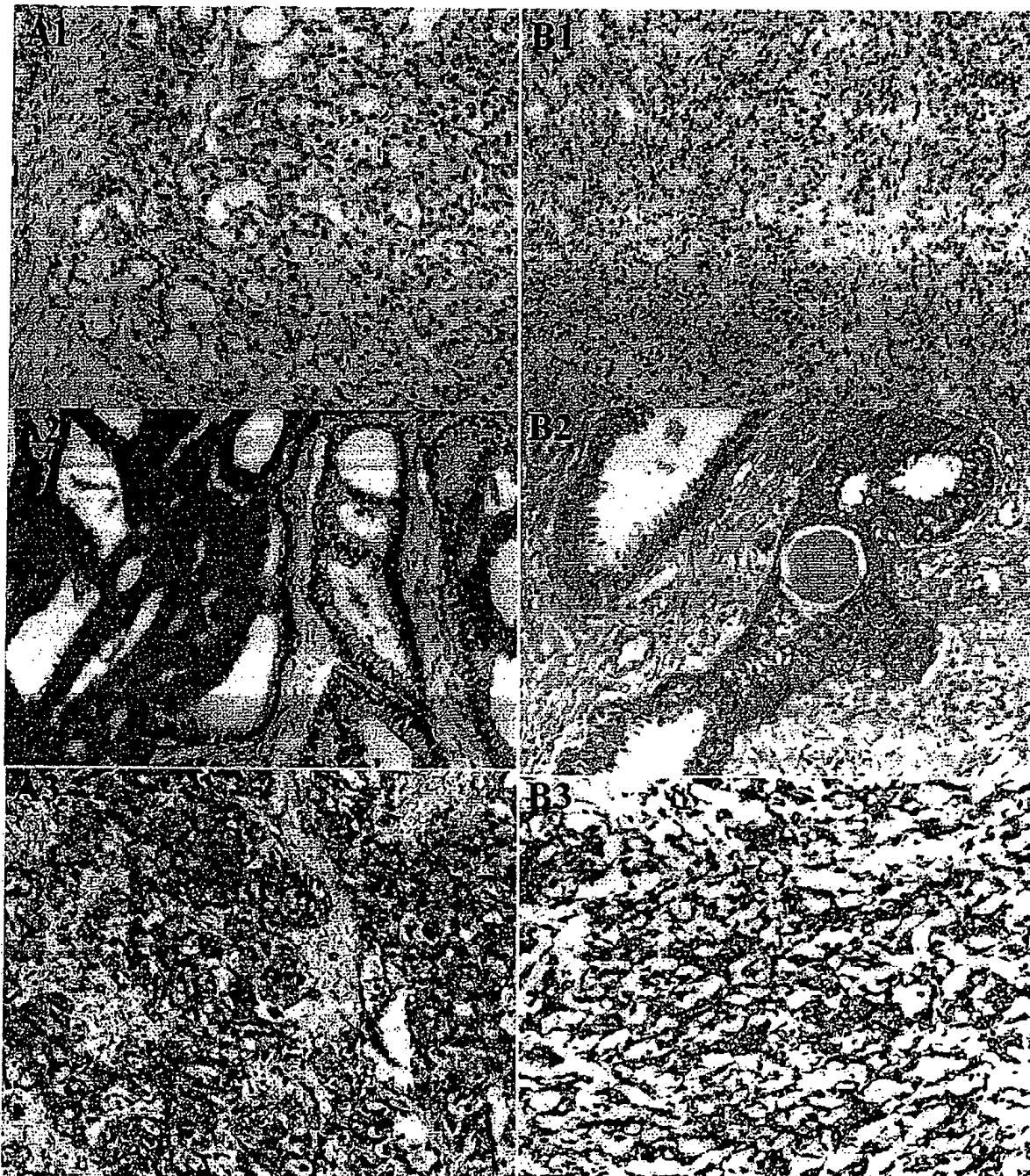


Figure 1

Representatives of PSA IHC and ISH staining in Pca (A. IHC staining, B. ISH staining, $\times 200$ magnification). A₁, B₁: negative control of IHC and ISH. PBS replacing the primary antibody (A₁) and hybridization with a sense PSA probe (B₁) showed no background staining. A₂, B₂: a moderately differentiated Pca (Gleason score = $3+3=6$) with moderate staining (composite score = 6) in all malignant cells; A₂: IHC shows not only cell surface but also apparent cytoplasmic staining of PSA protein. A₃, B₃: a poorly differentiated Pca (Gleason score = $4+4=8$) with very strong staining (composite score = 9) in all malignant cells.

Discussion

PSCA is homologous to a group of cell surface proteins that mark the earliest phase of hematopoietic development. PSCA mRNA expression is prostate-specific in normal male tissues and is highly up-regulated in both androgen-dependent and-independent Pca xenografts (LAPC-4 tumors). We hypothesize that PSCA may play a role in Pca tumorigenesis and progression, and may serve as a target for Pca diagnosis and treatment. In this study, IHC and ISH showed that in general there were weak or absent PSCA protein and mRNA expression in BPH and low grade PIN tissues. However, PSCA protein and mRNA are widely expressed in HGPIN, the putative precursor of invasive Pca, suggesting that up-regulation of PSCA is an early event in prostate carcinogenesis. Recently, Reiter RE et al [1], using ISH analysis, reported that 97 of 118 (82%) HGPIN specimens stained strongly positive for PSCA mRNA. A very similar finding was seen on mouse PSCA (mPSCA) expression in mouse HGPIN tissues by Tran C. P et al [8]. These data suggest that PSCA may be a new marker associated with transformation of prostate cells and tumorigenesis.

We observed that PSCA protein and mRNA are highly expressed in a large percentage of human prostate cancers, including advanced, poorly differentiated, androgen-independent and metastatic cases. Fluorescence-activated cell sorting and confocal/ immunofluorescent studies demonstrated cell surface expression of PSCA protein in Pca cells [9]. Our IHC expression analysis of PSCA shows not only cell surface but also apparent cytoplasmic staining of PSCA protein in Pca specimens (Figure 1). One possible explanation for this is that anti-PSCA antibody can recognize PSCA peptide precursors that reside in the cytoplasm. Also, it is possible that the positive staining that appears in the cytoplasm is actually from the overlying cell membrane [5]. These data seem to indicate that PSCA is a novel cell surface marker for human Pca.

Our results show that elevated level of PSCA expression correlates with high grade (i.e. poor differentiation), increased tumor stage and progression to androgen-independence of Pca. These findings support the original IHC analyses by Gu Z et al [9], who reported that PSCA protein expressed in 94% of primary Pca and the intensity of PSCA protein expression increased with tumor grade, stage and progression to androgen-independence. Our results also collaborate the recent work of Han KR et al [10], in which the significant association between high PSCA expression and adverse prognostic features such as high Gleason score, seminal vesicle invasion and capsular involvement in Pca was found. It is suggested that PSCA overexpression may be an adverse predictor for recurrence, clinical progression or survival of Pca. Hara H et al [11] used RT-PCR detection of PSA, PSMA and PSCA in 1

ml of peripheral blood to evaluate Pca patients with poor prognosis. The results showed that among 58 Pca patients, each PCR indicated the prognostic value in the hierarchy of PSCA>PSA>PSMA RT-PCR, and extraprostatic cases with positive PSCA PCR indicated lower disease-progression-free survival than those with negative PSCA PCR, demonstrating that PSCA can be used as a prognostic factor. Dubey P et al [12] reported that elevated numbers of PSCA + cells correlate positively with the onset and development of prostate carcinoma over a long time span in the prostates of the TRAMP and PTEN +/- models compared with its normal prostates. Taken together with our present findings, in which PSCA is overexpressed from HGPIN to almost frank carcinoma, it is reasonable and possible to use increased PSCA expression level or increased numbers of PSCA-positive cells in the prostate samples as a prognostic marker to predict the potential onset of this cancer. These data raise the possibility that PSCA may have diagnostic utility or clinical prognostic value in human Pca.

The cause of PSCA overexpression in Pca is not known. One possible mechanism is that it may result from PSCA gene amplification. In humans, PSCA is located on chromosome 8q24.2 [1], which is often amplified in metastatic and recurrent Pca and considered to indicate a poor prognosis [13-15]. Interestingly, PSCA is in close proximity to the c-myc oncogene, which is amplified in >20% of recurrent and metastatic prostate cancers [16,17]. Reiter RE et al [18] reported that PSCA and MYC gene copy numbers were co-amplified in 25% of tumors (five out of twenty), demonstrating that PSCA overexpression is associated with PSCA and MYC coamplification in Pca. Gu Z et al [9] recently reported that in 102 specimens available to compare the results of PSCA immunostaining with their previous mRNA ISH analysis, 92 (90.2%) had identically positive areas of PSCA protein and mRNA expression. Taken together with our findings, in which we detected moderate to strong expression of PSCA protein and mRNA in 34 of 40 (85%) Pca specimens examined simultaneously by IHC and ISH analyses, it is demonstrated that PSCA protein and mRNA overexpressed in human Pca, and that the increased protein level of PSCA was resulted from the upregulated transcription of its mRNA.

At present, the regulation mechanisms of human PSCA expression and its biological function are yet to be elucidated. PSCA expression may be regulated by multiple factors [18]. Watabe T et al [19] reported that transcriptional control is a major component regulating PSCA expression levels. In addition, induction of PSCA expression may be regulated or mediated through cell-cell contact and protein kinase C (PKC) [20]. Homologues of PSCA have diverse activities, and have themselves been involved in

carcinogenesis. Signalling through SCA-2 has been demonstrated to prevent apoptosis in immature thymocytes [21]. Thy-1 is involved in T cell activation and transduces signals through src-like tyrosine kinases [22]. Ly-6 genes have been implicated both in tumorigenesis and in cell-cell adhesion [23-25]. Cell-cell or cell-matrix interaction is critical for local tumor growth and spread to distal sites. From its restricted expression in basal cells of normal prostate and its homology to SCA-2, PSCA may play a role in stem/progenitor cell function, such as self-renewal (i.e. anti-apoptosis) and/or proliferation [1]. Taken together with the results in the present study, we speculate that PSCA may play a role in tumorigenesis and clinical progression of Pca through affecting cell transformation and proliferation. From our results, it is also suggested that PSCA as a new cell surface antigen may have a number of potential uses in the diagnosis, therapy and clinical prognosis of human Pca. PSCA overexpression in prostate biopsies could be used to identify patients at high risk to develop recurrent or metastatic disease, and to discriminate cancers from normal glands in prostatectomy samples. Similarly, the detection of PSCA-overexpressing cells in bone marrow or peripheral blood may identify and predict metastatic progression better than current assays, which identify only PSA-positive or PSMA-positive prostate cells.

In summary, we have shown in this study that PSCA protein and mRNA are maintained in expression from HGPIN through all stages of Pca in a majority of cases, which may be associated with prostate carcinogenesis and correlate positively with high tumor grade (poor cell differentiation), advanced stage and androgen-independent progression. PSCA protein overexpression is due to the upregulation of its mRNA transcription. The results suggest that PSCA may be a promising molecular marker for the clinical prognosis of human Pca and a valuable target for diagnosis and therapy of this tumor.

Competing interests

None declared.

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Review

Translation Initiation in Cancer: A Novel Target for Therapy¹

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Abstract

Translation initiation is regulated in response to nutrient availability and mitogenic stimulation and is coupled with cell cycle progression and cell growth. Several alterations in translational control occur in cancer. Variant mRNA sequences can alter the translational efficiency of individual mRNA molecules, which in turn play a role in cancer biology. Changes in the expression or availability of components of the translational machinery and in the activation of translation through signal transduction pathways can lead to more global changes, such as an increase in the overall rate of protein synthesis and translational activation of the mRNA molecules involved in cell growth and proliferation. We review the basic principles of translational control, the alterations encountered in cancer, and selected therapies targeting translation initiation to help elucidate new therapeutic avenues.

Introduction

The fundamental principle of molecular therapeutics in cancer is to exploit the differences in gene expression between cancer cells and normal cells. With the advent of cDNA array technology, most efforts have concentrated on identifying differences in gene expression at the level of mRNA, which can be attributable either to DNA amplification or to differences in transcription. Gene expression is quite complicated, however, and is also regulated at the level of mRNA stability, mRNA translation, and protein stability.

The power of translational regulation has been best recognized among developmental biologists, because transcription does not occur in early embryogenesis in eukaryotes. For example, in *Xenopus*, the period of transcriptional quiescence continues until the embryo reaches midblastula transition, the 4000-cell stage. Therefore, all necessary mRNA molecules are transcribed during oogenesis and stockpiled in a translationally inactive, masked form. The mRNA are translationally activated at appropriate times during oocyte maturation, fertilization, and

early embryogenesis and thus, are under strict translational control.

Translation has an established role in cell growth. Basically, an increase in protein synthesis occurs as a consequence of mitogenesis. Until recently, however, little was known about the alterations in mRNA translation in cancer, and much is yet to be discovered about their role in the development and progression of cancer. Here we review the basic principles of translational control, the alterations encountered in cancer, and selected therapies targeting translation initiation to elucidate potential new therapeutic avenues.

Basic Principles of Translational Control

Mechanism of Translation Initiation

Translation initiation is the main step in translational regulation. Translation initiation is a complex process in which the initiator tRNA and the 40S and 60S ribosomal subunits are recruited to the 5' end of a mRNA molecule and assembled by eukaryotic translation initiation factors into an 80S ribosome at the start codon of the mRNA (Fig. 1). The 5' end of eukaryotic mRNA is capped, i.e., contains the cap structure m⁷GpppN (7-methyl-guanosine-triphospho-5'-ribonucleoside). Most translation in eukaryotes occurs in a cap-dependent fashion, i.e., the cap is specifically recognized by the eIF4E,³ which binds the 5' cap. The eIF4F translation initiation complex is then formed by the assembly of eIF4E, the RNA helicase eIF4A, and eIF4G, a scaffolding protein that mediates the binding of the 40S ribosomal subunit to the mRNA molecule through interaction with the eIF3 protein present on the 40S ribosome. eIF4A and eIF4B participate in melting the secondary structure of the 5' UTR of the mRNA. The 43S initiation complex (40S/eIF2/Met-tRNA/GTP complex) scans the mRNA in a 5'→3' direction until it encounters an AUG start codon. This start codon is then base-paired to the anticodon of initiator tRNA, forming the 48S initiation complex. The initiation factors are then displaced from the 48S complex, and the 60S ribosome joins to form the 80S ribosome.

Unlike most eukaryotic translation, translation initiation of certain mRNAs, such as the picornavirus RNA, is cap independent and occurs by internal ribosome entry. This mechanism does not require eIF4E. Either the 43S complex can bind the initiation codon directly through interaction with the IRES in the 5' UTR such as in the encephalomyocarditis virus, or it can

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³The abbreviations used are: eIF4E, eukaryotic initiation factor 4E; UTR, untranslated region; IRES, internal ribosome entry site; 4E-BP1, eukaryotic initiation factor 4E-binding protein 1; S6K, ribosomal p70 S6 kinase; mTOR, mammalian target of rapamycin; ATM, ataxia telangiectasia mutated; PI3K, phosphatidylinositol 3-kinase; PTEN, phosphatase and tensin homolog deleted from chromosome 10; PP2A, protein phosphatase 2A; TGF- β 3, transforming growth factor- β 3; PAP, poly(A) polymerase; EPA, eicosapentaenoic acid; mda-7, melanoma differentiation-associated gene 7.

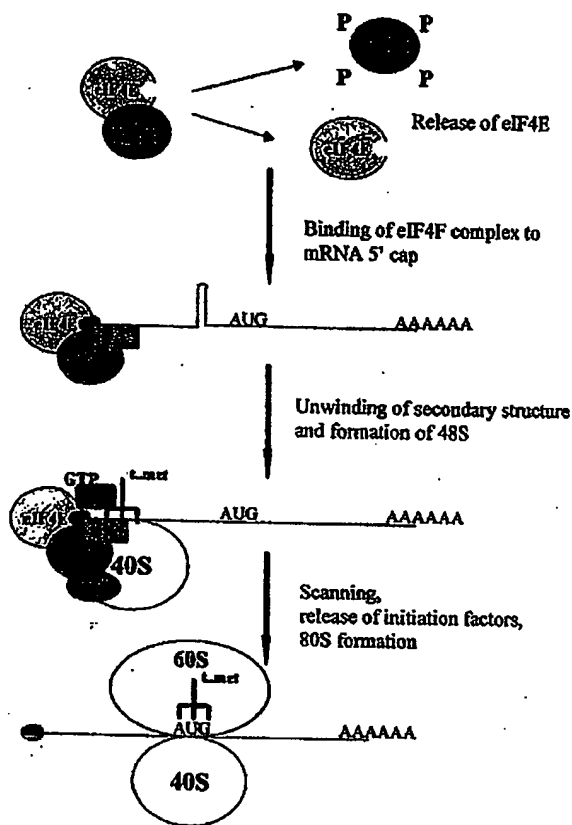


Fig. 1. Translation initiation in eukaryotes. The 4E-BPs are hyperphosphorylated to release eIF4E so that it can interact with the 5' cap, and the eIF4F initiation complex is assembled. The interaction of poly(A) binding protein with the initiation complex and circularization of the mRNA is not depicted in the diagram. The secondary structure of the 5' UTR is melted, the 40S ribosomal subunit is bound to eIF3, and the ternary complex consisting of eIF2, GTP, and the Met-tRNA are recruited to the mRNA. The ribosome scans the mRNA in a 5'→3' direction until an AUG start codon is found in the appropriate sequence context. The initiation factors are released, and the large ribosomal subunit is recruited.

Initially attach to the IRES and then reach the initiation codon by scanning or transfer, as is the case with the poliovirus (1).

Regulation of Translation Initiation

Translation initiation can be regulated by alterations in the expression or phosphorylation status of the various factors involved. Key components in translational regulation that may provide potential therapeutic targets follow.

eIF4E. eIF4E plays a central role in translation regulation. It is the least abundant of the initiation factors and is considered the rate-limiting component for initiation of cap-dependent translation. eIF4E may also be involved in mRNA splicing, mRNA 3' processing, and mRNA nucleocytoplasmic transport (2). eIF4E expression can be increased at the transcriptional level in response to serum or growth factors (3). eIF4E overexpression may cause preferential translation of mRNAs containing excessive secondary structure in their 5' UTR that are normally discriminated against by the trans-

lational machinery and thus are inefficiently translated (4-7). As examples of this, overexpression of eIF4E promotes increased translation of vascular endothelial growth factor, fibroblast growth factor-2, and cyclin D1 (2, 8, 9).

Another mechanism of control is the regulation of eIF4E phosphorylation. eIF4E phosphorylation is mediated by the mitogen-activated protein kinase-interacting kinase 1, which is activated by the mitogen-activated pathway activating extracellular signal-related kinases and the stress-activated pathway acting through p38 mitogen-activated protein kinase (10-13). Several mitogens, such as serum, platelet-derived growth factor, epidermal growth factor, insulin, angiotensin II, src kinase overexpression, and ras overexpression, lead to eIF4E phosphorylation (14). The phosphorylation status of eIF4E is usually correlated with the translational rate and growth status of the cell; however, eIF4E phosphorylation has also been observed in response to some cellular stresses when translational rates actually decrease (15). Thus, further study is needed to understand the effects of eIF4E phosphorylation on eIF4E activity.

Another mechanism of regulation is the alteration of eIF4E availability by the binding of eIF4E to the eIF4E-binding proteins (4E-BPs, also known as PHAS-I). 4E-BPs compete with eIF4G for a binding site in eIF4E. The binding of eIF4E to the best characterized eIF4E-binding protein, 4E-BP1, is regulated by 4E-BP1 phosphorylation. Hypophosphorylated 4E-BP1 binds to eIF4E, whereas 4E-BP1 hyperphosphorylation decreases this binding. Insulin, angiotensin, epidermal growth factor, platelet-derived growth factor, hepatocyte growth factor, nerve growth factor, insulin-like growth factors I and II, interleukin 3, granulocyte-macrophage colony-stimulating factor + steel factor, gastrin, and the adenovirus have all been reported to induce phosphorylation of 4E-BP1 and to decrease the ability of 4E-BP1 to bind eIF4E (15, 16). Conversely, deprivation of nutrients or growth factors results in 4E-BP1 dephosphorylation, an increase in eIF4E binding, and a decrease in cap-dependent translation.

p70 S6 Kinase. Phosphorylation of ribosomal 40S protein S6 by S6K is thought to play an important role in translational regulation. S6K $-/-$ mouse embryonic cells proliferate more slowly than do parental cells, demonstrating that S6K has a positive influence on cell proliferation (17). S6K regulates the translation of a group of mRNAs possessing a 5' terminal oligopyrimidine tract (5' TOP) found at the 5' UTR of ribosomal protein mRNAs and other mRNAs coding for components of the translational machinery. Phosphorylation of S6K is regulated in part based on the availability of nutrients (18, 19) and is stimulated by several growth factors, such as platelet-derived growth factor and insulin-like growth factor I (20).

eIF2 α Phosphorylation. The binding of the initiator tRNA to the small ribosomal unit is mediated by translation initiation factor eIF2. Phosphorylation of the α -subunit of eIF2 prevents formation of the eIF2/GTP/Met-tRNA complex and inhibits global protein synthesis (21, 22). eIF2 α is phosphorylated under a variety of conditions, such as viral infection, nutrient deprivation, heme deprivation, and apoptosis (22). eIF2 α is phosphorylated by heme-regulated inhibitor, nutrient-regulated protein kinase, and the IFN-induced, double-stranded RNA-activated protein kinase (PKR; Ref. 23).

The mTOR Signaling Pathway. The macrolide antibiotic rapamycin (Siralimus; Wyeth-Ayerst Research, Collegeville, PA) has been the subject of intensive study because it inhibits signal transduction pathways involved in T-cell activation. The rapamycin-sensitive component of these pathways is mTOR (also called FRAP or RAFT1). mTOR is the mammalian homologue of the yeast TOR proteins that regulate G₁ progression and translation in response to nutrient availability (24). mTOR is a serine-threonine kinase that modulates translation initiation by altering the phosphorylation status of 4E-BP1 and S6K (Fig. 2; Ref. 25).

4E-BP1 is phosphorylated on multiple residues. mTOR phosphorylates the Thr-37 and Thr-46 residues of 4E-BP1 *in vitro* (26); however, phosphorylation at these sites is not associated with a loss of eIF4E binding. Phosphorylation of Thr-37 and Thr-46 is required for subsequent phosphorylation at several COOH-terminal, serum-sensitive sites; a combination of these phosphorylation events appears to be needed to inhibit the binding of 4E-BP1 to eIF4E (25). The product of the ATM gene, p38/MSK1 pathway, and protein kinase C α also play a role in 4E-BP1 phosphorylation (27–29).

S6K and 4E-BP1 are also regulated, in part, by PI3K and its downstream protein kinase Akt. PTEN is a phosphatase that negatively regulates PI3K signaling. PTEN null cells have constitutively active Akt, with increased S6K activity and S6 phosphorylation (30). S6K activity is inhibited both by PI3K inhibitors wortmannin and LY294002 and by mTOR inhibitor rapamycin (24). Akt phosphorylates Ser-2448 in mTOR *in vitro*, and this site is phosphorylated upon Akt activation *in vivo* (31–33). Thus, mTOR is regulated by the PI3K/Akt pathway; however, this does not appear to be the only mode of regulation of mTOR activity. Whether the PI3K pathway also regulates S6K and 4E-BP1 phosphorylation independent of mTOR is controversial.

Interestingly, mTOR autophosphorylation is blocked by wortmannin but not by rapamycin (34). This seeming inconsistency suggests that mTOR-responsive regulation of 4E-BP1 and S6K activity occurs through a mechanism other than intrinsic mTOR kinase activity. An alternate pathway for 4E-BP1 and S6K phosphorylation by mTOR activity is by the inhibition of a phosphatase. Treatment with calyculin A, an inhibitor of phosphatases 1 and 2A, reduces rapamycin-induced dephosphorylation of 4E-BP1 and S6K by rapamycin (35). PP2A interacts with full-length S6K but not with a S6K mutant that is resistant to dephosphorylation resulting from rapamycin. mTOR phosphorylates PP2A *in vitro*; however, how this process alters PP2A activity is not known. These results are consistent with the model that phosphorylation of a phosphatase by mTOR prevents dephosphorylation of 4E-BP1 and S6K, and conversely, that nutrient deprivation and rapamycin block inhibition of the phosphatase by mTOR.

Polyadenylation. The poly(A) tail in eukaryotic mRNA is important in enhancing translation initiation and mRNA stability. Polyadenylation plays a key role in regulating gene expression during oogenesis and early embryogenesis. Some mRNA that are translationally inactive in the oocyte are polyadenylated concomitantly with translational activation in oocyte maturation, whereas other mRNAs that are translationally active during oogenesis are deadenylated and trans-

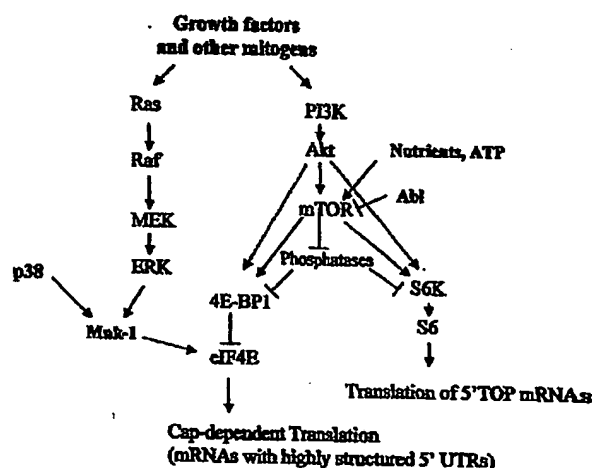


Fig. 2. Regulation of translation initiation by signal transduction pathways. Signaling via p38, extracellular signal-related kinase, PI3K, and mTOR can all activate translation initiation.

lationally silenced (36–38). Thus, control of poly(A) tail synthesis is an important regulatory step in gene expression. The 5' cap and poly(A) tail are thought to function synergistically to regulate mRNA translational efficiency (39, 40).

RNA Packaging. Most RNA-binding proteins are assembled on a transcript at the time of transcription, thus determining the translational fate of the transcript (41). A highly conserved family of Y-box proteins is found in cytoplasmic messenger ribonucleoprotein particles, where the proteins are thought to play a role in restricting the recruitment of mRNA to the translational machinery (41–43). The major mRNA-associated protein, YB-1, destabilizes the interaction of eIF4E and the 5' mRNA cap *in vitro*, and overexpression of YB-1 results in translational repression *in vivo* (44). Thus, alterations in RNA packaging can also play an important role in translational regulation.

Translation Alterations Encountered in Cancer

Three main alterations at the translational level occur in cancer: variations in mRNA sequences that increase or decrease translational efficiency, changes in the expression or availability of components of the translational machinery, and activation of translation through aberrantly activated signal transduction pathways. The first alteration affects the translation of an individual mRNA that may play a role in carcinogenesis. The second and third alterations can lead to more global changes, such as an increase in the overall rate of protein synthesis, and the translational activation of several mRNA species.

Variations in mRNA Sequence

Variations in mRNA sequence affect the translational efficiency of the transcript. A brief description of these variations and examples of each mechanism follow.

Mutations. Mutations in the mRNA sequence, especially in the 5' UTR, can alter its translational efficiency, as seen in the following examples.

c-myc. Salto *et al.* proposed that translation of full-length *c-myc* is repressed, whereas in several Burkitt lymphomas that have deletions of the mRNA 5' UTR, translation of *c-myc* is more efficient (45). More recently, it was reported that the 5' UTR of *c-myc* contains an IRES, and thus *c-myc* translation can be initiated by a cap-independent as well as a cap-dependent mechanism (46, 47). In patients with multiple myeloma, a C→T mutation in the *c-myc* IRES was identified (48) and found to cause an enhanced initiation of translation via internal ribosomal entry (49).

BRCA1. A somatic point mutation (117 G→C) in position -3 with respect to the start codon of the *BRCA1* gene was identified in a highly aggressive sporadic breast cancer (50). Chimeric constructs consisting of the wild-type or mutated *BRCA1* 5' UTR and a downstream luciferase reporter demonstrated a decrease in the translational efficiency with the 5' UTR mutation.

Cyclin-dependent Kinase Inhibitor 2A. Some inherited melanoma kindreds have a G→T transversion at base -34 of cyclin-dependent kinase inhibitor-2A, which encodes a cyclin-dependent kinase 4/cyclin-dependent kinase 6 kinase inhibitor important in G₁ checkpoint regulation (51). This mutation gives rise to a novel AUG translation initiation codon, creating an upstream open reading frame that competes for scanning ribosomes and decreases translation from the wild-type AUG.

Alternate Splicing and Alternate Transcription Start Sites. Alterations in splicing and alternate transcription sites can lead to variations in 5' UTR sequence, length, and secondary structure, ultimately impacting translational efficiency.

ATM. The *ATM* gene has four noncoding exons in its 5' UTR that undergo extensive alternative splicing (52). The contents of 12 different 5' UTRs that show considerable diversity in length and sequence have been identified. These divergent 5' leader sequences play an important role in the translational regulation of the *ATM* gene.

mdm. In a subset of tumors, overexpression of the oncoprotein *mdm2* results in enhanced translation of the *mdm2* mRNA. Use of different promoters leads to two *mdm2* transcripts that differ only in their 5' leaders (53). The longer 5' UTR contains two upstream open reading frames, and this mRNA is loaded with ribosomes inefficiently compared with the short 5' UTR.

BRCA1. In a normal mammary gland, *BRCA1* mRNA is expressed with a shorter leader sequence (5' UTRa), whereas in sporadic breast cancer tissue, *BRCA1* mRNA is expressed with a longer leader sequence (5' UTRb); the translational efficiency of transcripts containing 5' UTRb is 10 times lower than that of transcripts containing 5' UTRa (54).

TGF-β3. *TGF-β3* mRNA includes a 1.1-kb 5' UTR, which exerts an inhibitory effect on translation. Many human breast cancer cell lines contain a novel *TGF-β3* transcript with a 5' UTR that is 870 nucleotides shorter and has a 7-fold greater translational efficiency than the normal *TGF-β3* mRNA (55).

Alternate Polyadenylation Sites. Multiple polyadenylation signals leading to the generation of several transcripts with differing 3' UTR have been described for several mRNA species, such as the *RET* proto-oncogene (56), *ATM* gene (52), tissue inhibitor of metalloproteinases-3 (57), *RHOA*

proto-oncogene (58), and calmodulin-I (59). Although the effect of these alternate 3' UTRs on translation is not yet known, they may be important in RNA-protein interactions that affect translational recruitment. The role of these alterations in cancer development and progression is unknown.

Alterations in the Components of the Translation Machinery

Alterations in the components of translation machinery can take many forms.

Overexpression of eIF4E. Overexpression of eIF4E causes malignant transformation in rodent cells (60) and the deregulation of HeLa cell growth (61). Polunovsky *et al.* (62) found that eIF4E overexpression substitutes for serum and individual growth factors in preserving viability of fibroblasts, which suggests that eIF4E can mediate both proliferative and survival signaling.

Elevated levels of eIF4E mRNA have been found in a broad spectrum of transformed cell lines (63). eIF4E levels are elevated in all ductal carcinoma *in situ* specimens and invasive ductal carcinomas, compared with benign breast specimens evaluated with Western blot analysis (64, 65). Preliminary studies suggest that this overexpression is attributable to gene amplification (66).

There are accumulating data suggesting that eIF4E overexpression can be valuable as a prognostic marker. eIF4E overexpression was found in a retrospective study to be a marker of poor prognosis in stages I to III breast carcinoma (67). Verification of the prognostic value of eIF4E in breast cancer is now under way in a prospective trial (67). However, in a different study, eIF4E expression was correlated with the aggressive behavior of non-Hodgkin's lymphomas (68). In a prospective analysis of patients with head and neck cancer, elevated levels of eIF4E in histologically tumor-free surgical margins predicted a significantly increased risk of local-regional recurrence (9). These results all suggest that eIF4E overexpression can be used to select patients who might benefit from more aggressive systemic therapy. Furthermore, the head and neck cancer data suggest that eIF4E overexpression is a field defect and can be used to guide local therapy.

Alterations in Other Initiation Factors. Alterations in a number of other initiation factors have been associated with cancer. Overproduction of eIF4G, similar to eIF4E, leads to malignant transformation *in vitro* (69). eIF-2α is found in increased levels in bronchioloalveolar carcinomas of the lung (3). Initiation factor eIF-4A1 is overexpressed in melanoma (70) and hepatocellular carcinoma (71). The p40 subunit of translation initiation factor 3 is amplified and overexpressed in breast and prostate cancer (72), and the eIF3-p110 subunit is overexpressed in testicular seminoma (73). The role that overexpression of these initiation factors plays on the development and progression of cancer, if any, is not known.

Overexpression of S6K. S6K is amplified and highly overexpressed in the MCF7 breast cancer cell line, compared with normal mammary epithelium (74). In a study by Barlund *et al.* (74), S6K was amplified in 59 of 688 primary breast tumors, and a statistically significant association was observed between amplification and poor prognosis.

Overexpression of PAP. PAP catalyzes 3' poly(A) synthesis. PAP is overexpressed in human cancer cells compared with normal and virally transformed cells (75). PAP enzymatic activity in breast tumors has been correlated with PAP protein levels (76) and, in mammary tumor cytosols, was found to be an independent factor for predicting survival (76). Little is known, however, about how PAP expression or activity affects the translational profile.

Alterations in RNA-binding Proteins. Even less is known about alterations in RNA packaging in cancer. Increased expression and nuclear localization of the RNA-binding protein YB-1 are indicators of a poor prognosis for breast cancer (77), non-small cell lung cancer (78), and ovarian cancer (79). However, this effect may be mediated at least in part at the level of transcription, because YB-1 increases chemoresistance by enhancing the transcription of a multidrug resistance gene (80).

Activation of Signal Transduction Pathways

Activation of signal transduction pathways by loss of tumor suppressor genes or overexpression of certain tyrosine kinases can contribute to the growth and aggressiveness of tumors. An important mutant in human cancers is the tumor suppressor gene *PTEN*, which leads to the activation of the PI3K/Akt pathway. Activation of PI3K and Akt induces the oncogenic transformation of chicken embryo fibroblasts. The transformed cells show constitutive phosphorylation of S6K and of 4E-BP1 (81). A mutant Akt that retains kinase activity but does not phosphorylate S6K or 4E-BP1 does not transform fibroblasts, which suggests a correlation between the oncogenicity of PI3K and Akt and the phosphorylation of S6K and 4E-BP1 (81).

Several tyrosine kinases such as platelet-derived growth factor, insulin-like growth factor, HER2/neu, and epidermal growth factor receptor are overexpressed in cancer. Because these kinases activate downstream signal transduction pathways known to alter translation initiation, activation of translation is likely to contribute to the growth and aggressiveness of these tumors. Furthermore, the mRNA for many of these kinases themselves are under translational control. For example, HER2/neu mRNA is translationally controlled both by a short upstream open reading frame that represses HER2/neu translation in a cell type-independent manner and by a distinct cell type-dependent mechanism that increases translational efficiency (82). HER2/neu translation is different in transformed and normal cells. Thus, it is possible that alterations at the translational level can in part account for the discrepancy between *HER2/neu* gene amplification detected by fluorescence *in situ* hybridization and protein levels detected by immunohistochemical assays.

Translation Targets of Selected Cancer Therapy

Components of the translation machinery and signal pathways involved in the activation of translation initiation represent good targets for cancer therapy.

Targeting the mTOR Signaling Pathway: Rapamycin and Temstatin

Rapamycin inhibits the proliferation of lymphocytes. It was initially developed as an immunosuppressive drug for organ

transplantation. Rapamycin with FKBP 12 (FK506-binding protein, M_r 12,000) binds to mTOR to inhibit its function.

Rapamycin causes a small but significant reduction in the initiation rate of protein synthesis (83). It blocks cell growth in part by blocking S6 phosphorylation and selectively suppressing the translation of 5' TOP mRNAs, such as ribosomal proteins, and elongation factors (83–85). Rapamycin also blocks 4E-BP1 phosphorylation and inhibits cap-dependent but not cap-independent translation (17, 86).

The rapamycin-sensitive signal transduction pathway, activated during malignant transformation and cancer progression, is now being studied as a target for cancer therapy (87). Prostate, breast, small cell lung, glioblastoma, melanoma, and T-cell leukemia are among the cancer lines most sensitive to the rapamycin analogue CCI-779 (Wyeth-Ayerst Research; Ref. 87). In rhabdomyosarcoma cell lines, rapamycin is either cytostatic or cytotoxic, depending on the p53 status of the cell; p53 wild-type cells treated with rapamycin arrest in the G₁ phase and maintain their viability, whereas p53 mutant cells accumulate in G₁ and undergo apoptosis (88, 89). In a recently reported study using human primitive neuroectodermal tumor and medulloblastoma models, rapamycin exhibited more cytotoxicity in combination with cisplatin and camptothecin than as a single agent. *In vivo*, CCI-779 delayed growth of xenografts by 160% after 1 week of therapy and 240% after 2 weeks. A single high-dose administration caused a 37% decrease in tumor volume. Growth inhibition *in vivo* was 1.3 times greater, with cisplatin in combination with CCI-779 than with cisplatin alone (90). Thus, preclinical studies suggest that rapamycin analogues are useful as single agents and in combination with chemotherapy.

Rapamycin analogues CCI-779 and RAD001 (Novartis, Basel, Switzerland) are now in clinical trials. Because of the known effect of rapamycin on lymphocyte proliferation, a potential problem with rapamycin analogues is immunosuppression. However, although prolonged immunosuppression can result from rapamycin and CCI-779 administered on continuous-dose schedules, the immunosuppressive effects of rapamycin analogues resolve in ~24 h after therapy (91). The principal toxicities of CCI-779 have included dermatological toxicity, myelosuppression, infection, mucositis, diarrhea, reversible elevations in liver function tests, hyperglycemia, hypokalemia, hypocalcemia, and depression (87, 92–94). Phase II trials of CCI-779 have been conducted in advanced renal cell carcinoma and in stage III/IV breast carcinoma patients who failed with prior chemotherapy. In the results reported in abstract form, although there were no complete responses, partial responses were documented in both renal cell carcinoma and in breast carcinoma (94, 95). Thus, CCI-779 has documented preliminary clinical activity in a previously treated, unselected patient population.

Active investigation is under way into patient selection for mTOR inhibitors. Several studies have found an enhanced efficacy of CCI-779 in PTEN-null tumors (30, 86). Another study found that six of eight breast cancer cell lines were responsive to CCI-779, although only two of these lines lacked PTEN (97). There was, however, a positive correlation between Akt activation and CCI-779 sensitivity (97). This correlation suggests that activation of the PI3K-Akt pathway,

regardless of whether it is attributable to a PTEN mutation or to overexpression of receptor tyrosine kinases, makes cancer cell amenable to mTOR-directed therapy. In contrast, lower levels of the target of mTOR, 4E-BP1, are associated with rapamycin resistance; thus, a lower 4E-BP1/eIF4E ratio may predict rapamycin resistance (98).

Another mode of activity for rapamycin and its analogues appears to be through inhibition of angiogenesis. This activity may be both through direct inhibition of endothelial cell proliferation as a result of mTOR inhibition in these cells or by inhibition of translation of such proangiogenic factors as vascular endothelial growth factor in tumor cells (99, 100).

The angiogenesis inhibitor tumstatin, another anticancer drug currently under study, was also found recently to inhibit translation in endothelial cells (101). Through a requisite interaction with Integrin, tumstatin inhibits activation of the PI3K/Akt pathway and mTOR in endothelial cells and prevents dissociation of eIF4E from 4E-BP1, thereby inhibiting cap-dependent translation. These findings suggest that endothelial cells are especially sensitive to therapies targeting the mTOR-signaling pathway.

Targeting eIF2 α : EPA, Clotrimazole, mda-7, and Flavonoids

EPA is an n-3 polyunsaturated fatty acid found in the fish-based diets of populations having a low incidence of cancer (102). EPA inhibits the proliferation of cancer cells (103), as well as in animal models (104, 105). It blocks cell division by inhibiting translation initiation (105). EPA releases Ca²⁺ from intracellular stores while inhibiting their refilling, thereby activating PKR. PKR, in turn phosphorylates and inhibits eIF2 α , resulting in the inhibition of protein synthesis at the level of translation initiation. Similarly, clotrimazole, a potent antiproliferative agent *in vitro* and *in vivo*, inhibits cell growth through depletion of Ca²⁺ stores, activation of PKR, and phosphorylation of eIF2 α (106). Consequently, clotrimazole preferentially decreases the expression of cyclins A, E, and D1, resulting in blockage of the cell cycle in G₁.

mda-7 is a novel tumor suppressor gene being developed as a gene therapy agent. Adenoviral transfer of mda-7 (Ad-mda7) induces apoptosis in many cancer cells including breast, colorectal, and lung cancer (107–109). Ad-mda7 also induces and activates PKR, which leads to phosphorylation of eIF2 α and induction of apoptosis (110).

Flavonoids such as genistein and quercetin suppress tumor cell growth. All three mammalian eIF2 α kinases, PKR, heme-regulated inhibitor, and PERK/PEK, are activated by flavonoids, with phosphorylation of eIF2 α and inhibition of protein synthesis (111).

Targeting eIF4A and eIF4E: Antisense RNA and Peptides

Antisense expression of eIF4A decreases the proliferation rate of melanoma cells (112). Sequestration of eIF4E by overexpression of 4E-BP1 is proapoptotic and decreases tumorigenicity (113, 114). Reduction of eIF4E with antisense RNA decreases soft agar growth, increases tumor latency, and increases the rates of tumor doubling times (7). Antisense eIF4E RNA treat-

ment also reduces the expression of angiogenic factors (115) and has been proposed as a potential adjuvant therapy for head and neck cancers, particularly when elevated eIF4E is found in surgical margins. Small molecule inhibitors that bind the eIF4G/4E-BP1-binding domain of eIF4E are proapoptotic (116) and are also being actively pursued.

Exploiting Selective Translation for Gene Therapy

A different therapeutic approach that takes advantage of the enhanced cap-dependent translation in cancer cells is the use of gene therapy vectors encoding suicide genes with highly structured 5' UTR. These mRNA would thus be at a competitive disadvantage in normal cells and not translate well, whereas in cancer cells, they would translate more efficiently. For example, the introduction of the 5' UTR of fibroblast growth factor-2 5' to the coding sequence of *herpes simplex virus type-1 thymidine kinase* gene, allows for selective translation of *herpes simplex virus type-1 thymidine kinase* gene in breast cancer cell lines compared with normal mammary cell lines and results in selective sensitivity to ganciclovir (117).

Toward the Future

Translation is a crucial process in every cell. However, several alterations in translational control occur in cancer. Cancer cells appear to need an aberrantly activated translational state for survival, thus allowing the targeting of translation initiation with surprisingly low toxicity. Components of the translational machinery, such as eIF4E, and signal transduction pathways involved in translation initiation, such as mTOR, represent promising targets for cancer therapy. Inhibitors of the mTOR have already shown some preliminary activity in clinical trials. It is possible that with the development of better predictive markers and better patient selection, response rates to single-agent therapy can be improved. Similar to other cytostatic agents, however, mTOR inhibitors are most likely to achieve clinical utility in combination therapy. In the interim, our increasing understanding of translation initiation and signal transduction pathways promise to lead to the identification of new therapeutic targets in the near future.

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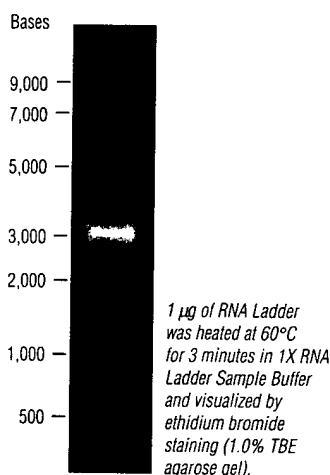
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RNA Ladder

#N0362S 25 µg \$55



Description: The RNA Ladder is a set of 7 RNA molecules produced by *in vitro* transcription of a mixture of 7 linear DNA templates. The ladder sizes are: 9000, 7000, 5000, 3000, 2000, 1000 and 500 bases. The 3000 base fragment is at double intensity to serve as a reference band. This ladder is suitable for use as an RNA size standard on denaturing or native agarose gels.

Reagents Supplied with Ladders:

2X RNA Ladder Sample Buffer (for use with native agarose gels)

2X RNA Ladder Sample Buffer:

2X TBE (pH 8.3), 13% ficoll (w/v), 0.01% bromophenol blue and 7 M urea.

Concentration: 500 µg/ml.

Storage Conditions: 20 mM KOAc (pH 4.5). Store at -70°C. For short term storage (< 1 week), ladder can be stored at -20°C.

Notes on Use:

To avoid ribonuclease contamination: wear gloves, use RNase-free water for gels and buffers, wash equipment with detergent and rinse thoroughly with RNase-free water.

It is best to use freshly poured gels that are as thin as possible (i.e., 2–10 mm). Excessively long run times or

high voltage can cause degradation of the bands on the gel. We recommend 4–8 volts/cm and running the bromophenol blue approximately 5 cm into the gel for good resolution.

Adding ethidium bromide to agarose gels and running buffer at a final concentration of 0.5 µg/ml will effectively stain the bands during electrophoresis.

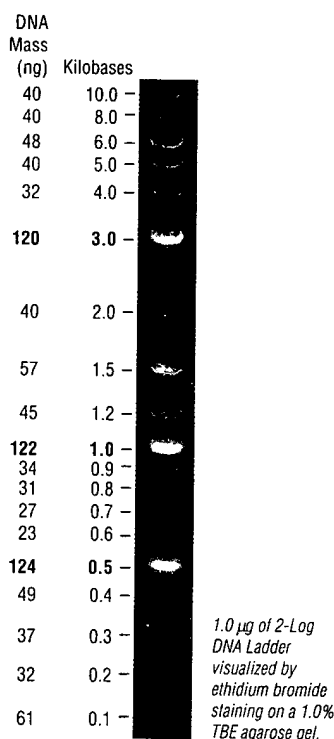
Denaturing vs. Native Agarose Gels:

It is common practice to electrophorese RNA on a fully denaturing agarose gel, such as one containing formaldehyde (1). However, in many cases it is possible to run RNA on a native agarose gel and obtain suitable results. In fact, it has been demonstrated that treatment of RNA samples in a denaturing buffer maintains the RNA molecules in a denatured state, during electrophoresis, for at least 3 hours (2,3). The use of native agarose gels eliminates problems associated with toxic chemicals and the difficulties encountered when staining and blotting formaldehyde gels.

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- (3) Sandra Cook and Christina Marchetti, unpublished observations.

2-Log DNA Ladder (0.1–10.0 kb)

#N3200S 100 µg \$55
#N3200L 500 µg \$220

Description: A number of proprietary plasmids are digested to completion with appropriate restriction enzymes to yield 19 bands suitable for use as molecular weight standards for agarose gel electrophoresis. This digested DNA includes fragments ranging from 100 bp to 10 kb. The 0.5, 1.0 and 3.0 kb bands have increased intensity to serve as reference points.

Preparation: Double-stranded DNA is digested to completion with the appropriate restriction enzymes, phenol extracted and equilibrated to 10 mM Tris-HCl (pH 8.0) and 1 mM EDTA.

Concentration: 1,000 µg/ml.

Storage Conditions: 10 mM Tris-HCl (pH 8.0) and 1 mM EDTA. For long term storage, store at -20°C. 2-Log DNA Ladder is stable for at least 3 months at 4°C.

Note: All fragments have 4-base, 5' overhangs that can be end labeled using T4 Polynucleotide Kinase (NEB #M0201) or filled-in using DNA Polymerase I, Klenow Fragment (NEB #M0210) (1). Use α-[³²P] dATP or α-[³²P] dTTP for the fill-in reaction.

Usage Recommendation: We recommend loading 1 µg of the 2-Log DNA Ladder diluted in sample buffer. This ladder was not designed for precise quantification of DNA mass but can be used for approximating the mass of DNA in comparably intense samples of similar size.

The approximate mass of DNA in each of the bands in our 2-Log DNA Ladder is as follows (assuming a 1 µg loading):

Fragment	Base Pairs	DNA Mass
1	10,002	40 ng
2	8,001	40 ng
3	6,001	48 ng
4	5,001	40 ng
5	4,001	32 ng
6	3,001	120 ng
7	2,017	40 ng
8	1,517	57 ng
9	1,200	45 ng
10	1,000	122 ng
11	900	34 ng
12	800	31 ng
13	700	27 ng
14	600	23 ng
15a	517	124 ng
15b	500	
16	400	49 ng
17	300	37 ng
18	200	32 ng
19	100	61 ng

Reference:

- (1) Sambrook, J., Fritsch, E. F. and Maniatis, T. (1989). *Molecular Cloning: A Laboratory Manual*, (2nd ed.), (pp. 10.51–10.67). Cold Spring Harbor: Cold Spring Harbor Laboratory Press.

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